

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1419	1btm		10	113	4.4e-11	-0.14	0.09		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	TYROSINE-PROTEIN KINASE
1419	1btm		8	112	1.2e-08	0.03	-0.01		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
1419	1fao	A	8	112	3.4e-20	0.64	0.80		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNAL TRANSDUCTION PROTEIN
1419	1fb8	A	8	112	3.4e-20	0.37	0.74		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1419	1pls		5	123	1.1e-18	0.34	0.35		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105- LEHHHHHH)) (NMR, 25	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN

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1419	1pls		7	118	3.4e-12	0.36	0.69		STRUCTURES) 1PLS 5 PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105- LEHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	
1419	1qgg	A	5	114	1e-16	0.40	0.90		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION
1419	1qgg	A	5	151	6.6e-23	0.06	0.30		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION
1420	1a06		118	203	1.3e-05	-0.47	0.31		CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1420	1a06		272	510	5.1e-78	0.65	0.77		CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1420	1a6o		279	511	6.8e-37	0.90	0.84		PROTEIN KINASE CK2/ALPHA- SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE- PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1420	1apm	E	118	198	1.1e-06	-0.19	0.10		TRANSFERASE/PHOSPHOTRANS FERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC	

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									SUBUNIT "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1420	1apm	E	213	518	0			88.91	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1420	1apm	E	248	513	0	0.60	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1420	1aq1		278	511	1e-51	0.69	0.93		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL

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										CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1420	1bi8	A	279	518	3.4e-44			62.61	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1420	1bi8	A	281	509	3.4e-44	0.37	0.36		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1420	1blx	A	281	511	3.4e-45	0.55	0.57		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA,

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										COMPLEX (INHIBITOR PROTEIN/KINASE)
1420	1cm8	A	295	511	1.5e-41	0.61	0.71		PHOSPHORYLATED MAP KINASE P38-GAMMA; CHAIN: A, B;	TRANSFERASE STRESS-ACTIVATED PROTEIN KINASE-3, ERK6, ERK5; P38-GAMMA, GAMMA, PHOSPHORYLATION, MAP KINASE
1420	1cmk	E	208	518	0			93.62	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1420	1cmk	E	243	513	0	0.63	0.98		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1420	1ctp	E	118	198	8.8e-07	-0.47	0.37		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1420	1ctp	E	210	518	0			97.24	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1420	1ctp	E	248	513	0	0.59	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	

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1420	1f3m	C	279	509	1.7e-52	0.73	0.86		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A; B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1420	1hcl		247	517	3.4e-53			62.10	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1420	1hcl		278	511	3.4e-53	0.49	0.98		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1420	1ian		278	515	1e-36	0.32	0.53		P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1420	1ir3	A	230	518	5.1e-26			75.00	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE

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										SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1420	ljnk		278	508	1.7e-40	0.65	0.94		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1420	lkoa		267	507	5.1e-62	0.67	0.48		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1420	lkob	A	273	510	1.2e-62	0.68	0.87		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1420	lp38		278	515	5.1e-43	0.57	0.43		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1420	lphk		118	203	6.6e-06	-0.39	0.03		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1420	lphk		250	512	5.1e-73			75.54	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE,

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										SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1420	1phk		277	509	5.1e-73	0.79	0.94		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1420	1pme		291	507	1.5e-37	0.58	0.43		ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1420	1tki	A	275	509	1.7e-48	0.65	0.49		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1420	3erk		281	507	6.8e-41	0.52	0.48		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1427	1a68		26	121	3.4e-26	0.34	0.98		POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION

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										DOMAIN, X-RAY 2 STRUCTURE, APLYSIA KV1.1
1427	1dsx	A	26	121	5.1e-25	0.28	0.75		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER
1427	1exb	E	26	123	1e-25	0.53	0.80		KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT
1427	1qdv	A	26	133	6.8e-27	0.26	0.82		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER
1427	1tld	A	26	134	1.7e-26	0.34	0.94		POTASSIUM CHANNEL KV1.1; CHAIN: A;	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KV1.1, PROTON TRANSPORT
1427	3kvt		27	136	1.5e-29	0.66	0.99		POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC- BINDING

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1430	1a5e		134	284	6e-25			61.39	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1430	1a5e		31	160	1.2e-30	0.44	0.92		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1430	1awc	B	10	164	1.2e-39	0.88	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	1awc	B	116	262	5.1e-37	0.54	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	1awc	B	149	291	5.1e-36	0.43	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR

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										PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	16	164	3.4e-34	0.91	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	182	299	8.5e-30	0.70	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	46	196	1.2e-39	0.96	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	46	198	1.5e-41			86.13	GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION

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									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	50	197	1.5e-39	1.09	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	8	131	1.2e-30	0.48	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	lawc	B	83	230	1.5e-41	1.00	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-

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										BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1430	1bd8		11	167	2.4e-40			82.84	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1430	1bd8		112	264	4.8e-34	0.67	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1430	1bd8		119	262	3.4e-28	0.49	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1430	1bd8		15	165	2.4e-40	0.53	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1430	1bd8		152	291	1.4e-29	0.84	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1430	1bd8		46	198	7.2e-38	0.78	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1430	1bd8		53	197	3.4e-33	0.86	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,

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1430	1bi7	B	144	267	2.4e-25			59.72	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	ANKYRIN MOTIF COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1430	1blx	B	10	171	5.1e-32			80.09	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1430	1blx	B	119	262	6.8e-27	0.54	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1430	1blx	B	152	291	3.4e-29	0.56	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN,

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										CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1430	1blx	B	53	197	5.1e-32	0.79	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D: CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1430	1bu9	A	116	267	1.7e-32	0.67	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1430	1bu9	A	149	297	1.7e-34	0.75	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1430	1bu9	A	50	202	8.5e-38	0.93	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1430	1bn9	A	8	176	8.5e-38			97.65	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1430	1d9s	A	35	169	3.6e-36	0.71	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1430	1d9s	A	9	136	1.1e-31	0.72	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1430	1ihb	A	10	168	3.6e-35	0.56	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1430	1ihb	A	116	266	8.5e-32	0.59	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1430	1ihb	A	12	168	3.4e-37			95.32	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	INHIBITOR CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1430	1ihb	A	149	296	8.5e-34	0.93	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1430	1ihb	A	50	201	3.4e-37	0.77	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1430	1ihb	A	81	232	2.4e-35	0.92	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1430	1ikn	D	11	181	3.4e-36	0.53	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1430	1ikn	D	111	282	1.7e-40	0.58	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	FACTOR, IKB/NFKB COMPLEX
1430	1ikn	D	144	300	1.5e-33	0.53	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1430	1ikn	D	45	230	8.5e-42	0.60	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1430	1ikn	D	45	251	8.5e-42			93.44	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1430	1myo		112	228	3.6e-30			71.55	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1430	1myo		147	293	6e-26	-0.12	0.10		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1430	1nfi	E	10	181	1e-36	0.68	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1430	1nfi	E	109	282	5.1e-40	0.94	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1430	1nfi	E	142	300	5.1e-33	0.68	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1430	1nfi	E	42	241	1.1e-47			94.63	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1430	1nfi	E	43	231	1.2e-46	0.88	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1430	1nfi	E	44	230	3.4e-42	0.77	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1430	1nfi	E	9	203	1.1e-47	0.80	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REPEAT), ANKYRIN 2 REPEAT HELIX
1430	1sw6	A	35	285	3.4e-18			66.83	REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1430	1ycs	B	47	235	3.4e-23			66.42	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1433	1a4y	A	153	410	3.4e-51	0.39	0.95		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1433	1a9n	A	226	397	4e-05	0.39	0.00		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1433	1a9n	C	223	375	1.8e-05	0.29	0.21		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1433	1ds9	A	224	345	0.0008	-0.32	0.05		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1433	1fqv	A	196	405	8e-12	0.29	0.70		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1433	1fqv	A	217	400	8.5e-11	0.19	0.53		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1433	1fs2	A	215	400	1.7e-11	-0.01	0.68		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1433	1yrg	A	194	407	2e-16	0.54	0.76		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1433	1yrg	A	197	409	5.1e-07	0.48	0.42		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1433	1yrg	A	217	374	1.2e-08	0.69	0.88		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TWINNING, MEROHEDRY TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDEAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1433	2bnh		153	410	5.1e-60	0.47	0.95		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1440	1a9n	B	13	79	3.6e-05	0.41	0.99		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1440	1cx0	A	13	79	0.00024	0.50	1.00		U1A PROTEIN; CHAIN: A; HDV RIBOZYME SELF-CLEAVED; CHAIN: B;	RNA BINDING PROTEIN/RNA NESTED DOUBLE PSEUDOKNOT RNA STRUCTURE
1440	1fht		13	79	3.6e-05	0.48	1.00		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1440	1ha1		13	84	0.0011	0.78	0.64		HNRNP A1; CHAIN: NULL;	DOMAIN, SPLICEOSOME
										NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1440	1nrc	A	13	79	0.00012	-0.21	0.77		RIBONUCLEOPROTEIN PROTEIN FROM U1 SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	
1440	1nrc	B	13	78	8.4e-05	-0.06	0.58		RIBONUCLEOPROTEIN PROTEIN FROM U1 SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	
1440	1urn	A	13	79	0.00024	0.72	0.98		U1A SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 2IMER HAIRPIN (5'-(AP*AP*Up*CP*CP*AP*Up*Up*(AP*AP*Up*CP*CP*AP*Up*Up*1URN 11 CHAIN: P, Q, R, 1URN 13	COMPLEX (RIBONUCLEOPROTEIN/RNA)
1440	2u1a		9	82	0.00012	0.34	0.04		U1 SMALL NUCLEAR	NUCLEAR PROTEIN U1

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBONUCLEOPROTEIN A; CHAIN: NULL;	SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
1440	2up1	A	14	84	0.0024	0.43	0.49		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1446	1a1h	A	10	78	8.8e-29	0.14	0.72		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1446	1a1h	A	134	215	8.8e-44	0.02	0.98		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1446	1a1h	A	302	382	8.5e-31	0.31	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1446	1a1h	A	302	383	6.6e-44	0.13	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1446	1alh	A	330	412	6.6e-44			80.03	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	PROTEIN
1446	1alh	A	4	77	5.1e-26	-0.28	0.71		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1446	1alh	A	81	187	4.4e-36	-0.01	0.48		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1446	1mey	C	109	186	3.4e-43	-0.08	0.93		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	133	214	1.2e-47	0.33	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	161	242	1.5e-49	0.42	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	189	270	5.1e-50	0.45	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	189	271	8.5e-51			100.67	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	217	298	8.5e-51	0.45	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	24	105	5.1e-45	0.38	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	245	326	3.4e-50	0.34	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	273	354	6.8e-50	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	3	77	8.5e-40	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	301	382	5.1e-50	-0.02	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1446	1mey	C	329	410	3.4e-50	0.19	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	52	130	6.8e-42	0.18	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	C	81	186	2.2e-37	-0.26	0.82		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1mey	G	22	49	5.1e-11	0.37	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1446	1tff	A	10	214	1.1e-56	-0.40	0.69		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	113	251	8.5e-35	-0.07	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	133	299	6.6e-72			112.82	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	134	326	6.6e-72	-0.10	0.72		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	218	410	2.2e-75	-0.34	0.70		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	246	392	1.7e-38	-0.29	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	274	410	8.5e-36	0.01	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	3	144	8.5e-33	-0.21	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1tf6	A	81	270	2.2e-71	-0.08	1.00		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1446	1ubd	C	10	105	6.6e-38	0.16	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	106	242	8.8e-48	-0.07	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	133	243	1.5e-57			89.69	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	159	270	1.5e-57	0.29	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	215	326	6.6e-54	-0.07	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	243	382	1.8e-52	0.05	0.34		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	278	382	3.4e-36	-0.08	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	299	410	6.6e-56	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	309	410	1.2e-34	0.17	0.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	32	130	1.7e-30	-0.05	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	4	105	3.4e-31	0.19	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	1ubd	C	50	186	2.2e-45	-0.09	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1446	2gli	A	113	241	1e-33	-0.09	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1446	2gli	A	133	272	1.1e-71			101.80	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1446	2gli	A	134	272	1.1e-71	0.61	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	BINDING PROTEIN/DNA)
1446	2gli	A	190	356	8.8e-70	0.03	0.88		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1446	2gli	A	24	188	8.8e-58	0.08	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1446	2gli	A	245	411	1.3e-72	0.12	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1446	2gli	A	253	381	1.7e-34	0.23	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1446	2gli	A	281	409	1.2e-34	0.15	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1446	2gli	A	4	132	3.4e-30	0.07	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1447	1avl	A	61	255	1.2e-09			60.91	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1447	1dn1	B	85	197	3.6e-08	0.16	-0.11		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS S NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1447	1qsa	A	60	313	7.2e-12	0.01	-0.13		SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA-SUPERHELIX, TRANSFERASE
1447	1quu	A	84	200	2.4e-09	0.17	-0.18		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1448	1avl	A	15	232	1.2e-09			61.06	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1448	1dn1	B	85	197	3.6e-08	0.16	-0.11		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1448	1qqe	A	84	318	0.00036	-0.09	0.07		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1448	1qsa	A	60	319	2.4e-12	0.10	-0.09		SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA-SUPERHELIX, TRANSFERASE
1451	1alh	A	70	150	3.4e-23	-0.53	0.23		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1451	1mey	C	125	206	3.4e-42	0.31	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	153	234	8.5e-44	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	181	262	1e-44	0.58	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	209	290	1.2e-45	-0.03	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	237	318	1.4e-46	0.15	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	265	346	3.4e-47	0.40	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	293	374	1.4e-48	0.73	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	321	402	1.7e-49	0.11	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	349	430	5.1e-50	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	377	458	5.1e-50	0.42	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	405	486	1e-50	0.75	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	1mey	C	433	514	6.8e-50	0.53	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	461	542	8.5e-51	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	461	543	8.5e-51			105.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	489	570	1.4e-50	0.47	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	517	598	1.4e-50	0.25	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	545	603	5.1e-35	0.05	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	69	150	3.4e-40	-0.42	0.31		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	C	97	178	3.4e-41	-0.37	0.92		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1mey	G	515	542	1.2e-13	1.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	1mey	G	515	542	3.4e-13	1.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1451	1tf6	A	126	276	1.7e-34	0.02	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1tf6	A	126	318	4.8e-60	-0.13	0.68		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1tf6	A	182	331	1.7e-36	0.11	0.95		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	1ff6	A	266	430	8.4e-71	-0.07	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1ff6	A	294	439	3.4e-37	0.27	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1ff6	A	378	523	1.7e-37	0.01	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1ff6	A	406	570	3.6e-72	-0.04	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	1tf6	A	434	580	5.1e-37	0.13	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	INITIATION, ZINC FINGER PROTEIN
1451	1tf6	A	434	596	3.6e-72			113.45	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1tf6	A	434	598	4.8e-69	0.05	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1tf6	A	462	600	8.5e-38	0.30	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1ff6	A	70	220	1.7e-33	-0.21	0.95		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1451	1ubd	C	125	234	3.6e-44	0.17	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	128	234	8.5e-30	-0.01	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	156	262	1.5e-30	0.06	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	158	262	1.1e-47	0.20	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	235	346	2.4e-51	0.32	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	273	374	6.8e-33	0.30	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	1ubd	C	319	430	7.2e-53	0.20	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	321	431	3.6e-54			94.56	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	329	430	5.1e-35	0.42	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	375	486	3.6e-54	0.14	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	385	486	1.2e-34	-0.16	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	413	514	3.4e-35	0.46	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	459	570	1.2e-53	0.20	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	469	570	1.7e-34	0.31	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	487	598	6e-51	0.22	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	1ubd	C	497	598	3.4e-34	0.29	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	1ubd	C	72	178	1.5e-28	-0.46	0.57		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1451	2gli	A	125	292	2.4e-63	0.25	0.21		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1451	2gli	A	153	289	1e-31	0.39	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1451	2gli	A	181	320	2.4e-65			96.49	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1451	2gli	A	181	348	2.4e-65	0.17	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1451	2gli	A	293	460	3.6e-68	-0.02	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1451	2gli	A	301	429	1.7e-33	0.41	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1451	2gli	A	405	572	1.2e-68	0.22	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1451	2gli	A	413	541	3.4e-34	0.29	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1451	2gli	A	441	569	1e-33	0.38	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1451	2gli	A	469	600	1.7e-34	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1451	2gli	A	49	177	5.1e-27	-0.26	0.19		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1451	2gli	A	72	236	4.8e-46	-0.16	0.24		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1456	1dbu	A	13	116	1.2e-06	0.61	1.00		YBAK; CHAIN: A;	STRUCTURAL GENOMICS, UNKNOWN FUNCTION HI1434; STRUCTURAL GENOMICS, UNKNOWN FUNCTION, HYPOTHETICAL PROTEIN, 2 YBAK
1459	1a4y	A	15	262	2.4e-32	0.77	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1459	1a4y	A	16	305	5.1e-28	0.43	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1459	1a4y	A	3	172	1.7e-13	0.49	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	MAPPING, LEUCINE-RICH 3 REPEATS COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1459	1a9n	A	61	178	1.1e-06	0.15	0.74		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1459	1a9n	A	88	212	9.6e-10	-0.00	0.69		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1459	1a9n	C	88	212	2.4e-09	0.20	0.53		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1459	1av1	A	247	447	1.1e-10			77.54	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1459	1cum	A	212	431	2.4e-14			76.97	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1459	1d0b	A	24	210	2.4e-06	0.09	0.89		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCTUM BINDING, CELL ADHESION
1459	1fo1	B	47	126	0.0017	-0.20	0.07		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1459	1fs2	A	35	211	2.4e-10	-0.16	0.27		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1459	1quu	A	214	455	1.2e-15			77.32	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1459	1yrg	A	10	267	6.8e-20	0.63	1.00		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	COIL, CONTRACTILE PROTEIN
1459	2bnh		7	282	1.2e-29	0.38	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGEN IN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1462	1cmk	E	170	504	3.4e-57	-0.02	0.03		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1462	1p38		179	514	1.7e-70	0.08	0.15		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1462	1phk		190	507	6.8e-59	0.06	-0.14		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1465	1cun	A	523	669	4.8e-05	-0.11	0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1465	1cun	A	630	851	6e-14	0.06	0.07		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1465	1cun	A	690	909	9.6e-16	-0.03	0.11		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1465	1cun	A	727	928	1.2e-15	0.24	-0.07		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1465	1cun	A	743	981	3.6e-27	0.26	0.11		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1465	1cun	A	873	1073	4.8e-16	0.19	-0.05		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1465	1dn1	B	878	1071	3.6e-14	0.05	-0.11		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS S NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1465	1fio	A	711	859	2.4e-12	0.24	-0.13		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1465	1qu7	A	646	864	4.8e-11	0.08	-0.15		METHYL-ACCEPTING CHEMOTAXIS PROTEIN I; CHAIN: A, B;	SIGNALING PROTEIN SERINE, CHEMOTAXIS, FOUR HELICAL-BUNDLE
1465	1quu	A	739	989	1.2e-28	0.11	-0.06		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1471	1a0j	A	64	298	0			242.91	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1471	1a0j	A	64	298	0	0.85	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1471	1a0l	A	64	298	3.4e-84			172.90	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1471	1a05	A	64	298	7.2e-93			216.40	GLANDULAR KALLIKREIN-13; CHAIN: A, B;	SERINE PROTEASE PRORENIN CONVERTING ENZYME (PRECE), EPIDERMAL GLANDULAR KALLIKREIN, SERINE PROTEASE, PROTEIN MATURATION
1471	1a05	A	67	298	7.2e-93	0.90	1.00		GLANDULAR KALLIKREIN-13; CHAIN: A, B;	SERINE PROTEASE PRORENIN CONVERTING ENZYME (PRECE), EPIDERMAL GLANDULAR KALLIKREIN, SERINE PROTEASE, PROTEIN MATURATION
1471	1aut	C	64	296	2.4e-85			182.46	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1471	1azz	A	64	298	3.4e-73			172.65	COLLAGENASE; CHAIN: A, B; ECOTIN; CHAIN: C, D;	COMPLEX (SERINE PROTEASE/INHIBITOR); TRYPSIN INHIBITOR; COMPLEX (SERINE PROTEASE/INHIBITOR), SERINE PROTEASE, 2 INHIBITOR, COMPLEX, PROTEASE-SUBSTRATE INTERACTIONS, 3 COLLAGEN
1471	1bio		64	296	2.4e-87			192.38	COMPLEMENT FACTOR D; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, HYDROLASE, COMPLEMENT, FACTOR D, CATALYTIC 2 TRIAD, SELF-REGULATION
1471	1bqy	A	64	298	3.4e-86			198.63	PLASMINOGEN ACTIVATOR; CHAIN: A, B; GLU-GLY-ARG-CHLOROMETHYLKETONE INHIBITOR; CHAIN: E, F;	BLOOD CLOTTING TSV-PA; FIBRINOLYSIS, PLASMINOGEN ACTIVATOR, SERINE PROTEINASE, 2 SNAKE VENOM, COMPLEX (HYDROLASE/INHIBITOR), BLOOD CLOTTING
1471	1bru	P	64	298	9.6e-83			169.32	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1471	1cgh	A	64	297	6.8e-74			174.24	CATHEPSIN G; CHAIN: A;	COMPLEX (SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PHOSPHONATE INHIBITOR SUC-VAL-PRO-PHEP-(OPH)2; CHAIN: S;	PROTEASE/INHIBITOR) INFLAMMATION, INHIBITOR, SPECIFICITY, SERINE PROTEASE, 2 COMPLEX (SERINE PROTEASE/INHIBITOR)
1471	1dpo		64	298	5.1e-99			234.19	TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
1471	1ekb	B	64	296	1.7e-79			170.43	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR
1471	1fxy	A	64	298	1.5e-90			217.83	COAGULATION FACTOR XA- TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG- CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
1471	1gct	A	54	298	6.8e-81			175.31	HYDROLASE (SERINE PROTEINASE) GAMMA-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									*CHYMOTRYPSIN *A (E.C.3.4.21.1) (SP*H 7.0) 1GCT 3	
1471	1mct	A	64	298	0			243.02	COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	
1471	1mct	A	64	298	0	0.99	1.00		COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	
1471	1nrm	A	64	296	3.6e-90			255.96	NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
1471	1qrz	A	45	298	1.7e-86			171.93	PLASMINOGEN; CHAIN: A, B, C, D;	HYDROLASE MICROPLASMINOGEN, SERINE PROTEASE, ZYMOGEN, CHYMOTRYPSIN 2 FAMILY, HYDROLASE
1471	1sgf	A	73	298	7.2e-79			183.53	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1471	1sgf	G	64	298	1.2e-94			234.25	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1471	1sgf	G	64	298	1.2e-94	0.89	1.00		NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	PROTEINASE (ALPHA-NGF) GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1471	1slw	B	64	298	0			224.62	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
1471	1slw	B	64	298	0	0.86	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
1471	1ton		64	298	1.1e-91			210.31	HYDROLASE(SERINE PROTEINASE) TONIN (E.C. NUMBER NOT ASSIGNED) 1TON 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1471	1ton		67	298	1.1e-91	0.87	1.00		HYDROLASE(SERINE PROTEINASE) TONIN (E.C. NUMBER NOT ASSIGNED) 1TON ₄	
1471	1tm	A	64	298	0			234.44	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHORFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
1471	1tm	A	64	298	0	0.92	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHORFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
1471	2tbs		64	296	0	0.85	1.00		HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS ₃	
1471	2tbs		64	298	0			235.83	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS ₃	
1471	5ptp		64	298	1.7e-			235.23	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
					100					HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1471	5ptp		64	298	1.7e-100	0.93	1.00		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1478	1a1h	A	349	412	3.4e-15	-0.06	0.58		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1478	1a1h	A	356	440	1.2e-28	0.36	0.96		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1478	1a1h	A	386	468	3.4e-31	0.18	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1478	1a1h	A	386	470	3.4e-31			70.55	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1478	1a1h	A	416	499	1.7e-27	0.08	0.81		QGSZ ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1478	1alh	A	444	504	8.5e-19	-0.36	0.22		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1478	1bbo		418	471	4.8e-16	-0.27	0.58		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 IBBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) IBBO 4	
1478	1mey	C	348	412	3.4e-28	-0.27	0.57		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1mey	C	354	440	6.8e-45	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1mey	C	385	468	1e-47	0.23	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1mey	C	385	469	1e-47			65.65	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1mey	C	415	498	5.1e-47	0.02	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1mey	C	443	504	6.8e-32	-0.30	0.16		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1mey	G	383	412	3.4e-11	0.44	0.69		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1478	1mey	G	441	468	1e-12	-0.33	0.45		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1sp2		386	416	6.8e-09	0.05	0.58		SPIF2; CHAIN: NULL;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1478	1tf3	A	348	412	1.7e-15	0.20	0.17		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	ZINC FINGER TRANSCRIPTION FACTOR SPI1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI1 COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1478	1tf3	A	355	440	8.5e-23	0.26	0.77		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1478	1tf3	A	416	499	6.8e-20	-0.25	0.35		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1478	1tf3	A	444	503	1.2e-13	-0.23	0.03		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1478	1tf6	A	325	499	1.7e-37			71.55	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1478	1tf6	A	355	501	1.7e-37	-0.12	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1478	1ubd	C	351	412	5.1e-20	0.07	0.60		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1478	1ubd	C	359	468	4.8e-26	0.09	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1478	1ubd	C	361	440	5.1e-29	-0.42	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1478	1ubd	C	387	499	3.4e-34			75.80	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1478	1ubd	C	390	498	3.4e-34	-0.04	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1478	1ubd	C	423	504	1.7e-25	-0.10	0.57		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1478	2adr		418	470	1e-15	-0.18	0.99		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1478	2adr		444	501	3.4e-15	-0.02	0.24		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1478	2gli	A	350	467	1.2e-33	0.21	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1478	2gli	A	356	500	1.7e-36			74.47	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1478	2gli	A	359	499	1.7e-36	0.27	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1488	1alh	A	294	378	2.4e-35	0.35	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1488	1alh	A	294	380	2.4e-35			87.16	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1488	1alh	A	296	378	1.2e-29	0.47	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1488	1alh	A	324	395	5.1e-27	0.17	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1488	1d0s	A	32	291	1.2e-09	0.03	-0.14		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1488	1mey	C	293	379	1.4e-51			94.84	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1488	1mey	C	295	378	1.4e-51	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1488	1mey	C	323	398	1e-43	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1488	1tf3	A	293	382	5.1e-21			73.75	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1488	1tf6	A	240	398	1e-25			61.08	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1488	1ubd	C	269	379	6.8e-31			80.80	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1488	1ubd	C	296	378	6.8e-31	0.30	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1488	1ubd	C	301	398	1.2e-28	0.11	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1488	2gli	A	237	380	2.4e-31			78.30	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1488	2gli	A	271	378	2.4e-31	0.38	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1488	2gli	A	295	377	3.4e-26	0.52	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1488	2gli	A	313	398	1.7e-26	0.04	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1489	lawc	A	111	224	3.4e-33			53.03	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1489	lawc	A	114	224	3.4e-33	0.88	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1489	1etc		114	220	6.8e-36	0.47	0.99		MURINE ETS-1 TRANSCRIPTION FACTOR; IETC 4 CHAIN: NULL; IETC 5	TRANSCRIPTION REGULATION
1489	1fli	A	106	204	3.4e-32			59.75	FLI-1; IFLI 5 CHAIN: A; IFLI 6 DNA IFLI 10 CHAIN: B, C; IFLI 12	COMPLEX (TRANSCRIPTION FACTOR/DNA)
1489	1fli	A	114	203	3.4e-32	0.27	0.96		FLI-1; IFLI 5 CHAIN: A; IFLI 6 DNA IFLI 10 CHAIN: B, C; IFLI 12	COMPLEX (TRANSCRIPTION FACTOR/DNA)
1489	1pue	E	110	197	8.5e-32			92.89	DNA (16 BASE PAIRS); CHAIN: A, B, C, D; TRANSCRIPTION FACTOR PU.1; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATING/DNA) PU.1; COMPLEX (TRANSCRIPTION REGULATING/DNA), ONCOGENE, 2 TRANSFORMING PROTEIN, DNA-BINDING, ACTIVATOR, 3 NUCLEAR PROTEIN
1489	1pue	E	114	197	8.5e-32	0.86	1.00		DNA (16 BASE PAIRS); CHAIN: A, B, C, D; TRANSCRIPTION FACTOR PU.1; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATING/DNA) PU.1; COMPLEX (TRANSCRIPTION REGULATING/DNA), ONCOGENE, 2 TRANSFORMING PROTEIN, DNA-BINDING, ACTIVATOR, 3 NUCLEAR PROTEIN
1495	1bj6	A	106	129	0.00024	-0.57	0.45		DNA (ACGCC); CHAIN: D; NUCLEOCAPSID PROTEIN 7; CHAIN: A;	COMPLEX (NUCLEOCAPSID PROTEIN/DNA) (12-53)NCP7; COMPLEX (NUCLEOCAPSID PROTEIN/DNA), NUCLEIC ACID, 2 RETROVIRUS,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										VIRUS MORPHOGENESIS, ZINC FINGER
1497	1ahd	P	237	302	1.7e-35	-0.14	0.99		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1497	1ahd	P	237	307	1.7e-35			66.86	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1497	1b72	A	231	298	8.5e-28			59.01	HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1497	1b72	A	241	298	8.5e-28	0.01	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1497	1d0s	A	71	243	4.4e-12	0.58	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL
1497	1ftz		235	309	1e-30			59.28	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN)	TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1497	1ftz		237	296	1e-30	-0.04	0.98		(NMR, 20 STRUCTURES) IFTZ 3 DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN)	
1497	1nk2	P	229	307	1.5e-17			55.18	(NMR, 20 STRUCTURES) IFTZ 3 HOMEODOMAIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)
1497	1nk2	P	234	302	1.5e-17	-0.33	0.99		HOMEODOMAIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)
1497	1osm	A	77	244	1.5e-08	0.65	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1497	1qry	A	226	307	6.8e-17			54.12	HOMEODOMAIN VENTRAL NERVOUS SYSTEM DEFECTIVE	DNA-BINDING PROTEIN HELIX-TURN-HELIX, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1497	1qry	A	234	302	6.8e-17	-0.19	0.72		CHAIN: A; HOMEODOMAIN VENTRAL NERVOUS SYSTEM DEFECTIVE CHAIN: A;	BINDING PROTEIN DNA-BINDING PROTEIN HELIX-TURN-HELIX, DNA-BINDING PROTEIN
1497	1san		242	302	3.4e-33	-0.24	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1497	1san		243	307	3.4e-33			61.49	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1497	9ant	A	241	296	1.7e-32			62.80	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1497	9ant	A	241	296	1.7e-32	0.07	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1501	1ahd	P	82	147	5.1e-31	0.24	0.90		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									(HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1501	1b72	A	86	142	1.7e-26	0.76	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1501	1bw5		82	143	2e-29	0.17	0.24		INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LJM DOMAIN
1501	1fjl	A	81	141	1.4e-27	0.23	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA- BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1501	1fjl	A	81	145	4e-28			58.65	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA- BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1501	1fjl	A	82	142	4e-28	0.18	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA- BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1501	1fjl	B	82	138	6e-27			55.11	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1501	1fjl	B	82	139	3.4e-26	0.33	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1501	1fjl	B	82	139	6e-27	0.33	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1501	1san		88	147	1.2e-28	0.48	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1502	1ez3	A	39	91	0.006	-0.27	0.03		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1508	1ahd	P	16	80	1.7e-31	0.12	0.98		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1508	1b72	A	20	77	3.4e-26	0.33	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1508	1b8i	A	20	74	5.1e-27	0.71	1.00		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1508	1ftt		16	82	3.4e-25	0.66	0.99		THYROID TRANSCRIPTION FACTOR 1 HOMEODOMAIN; 1FTT 6 CHAIN: NULL; 1FTT 7	DNA BINDING PROTEIN TTF-1 HD; 1FTT 8 DNA BINDING PROTEIN, HOMEODOMAIN, TRANSCRIPTION FACTOR 1FTT 19
1508	1ftz		17	75	1.2e-26	-0.06	1.00		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1508	1nk2	P	9	78	1.7e-25	0.50	0.99		HOMEODOMAIN PROTEIN VND; CHAIN: P; DNA; CHAIN: A; B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)
1508	1nk3	P	15	77	3.4e-24	0.43	0.93		HOMEODOMAIN VENTRAL; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA) HELIX
1508	1qry	A	6	78	6.8e-25	0.39	0.83		HOMEODOMAIN VENTRAL NERVOUS SYSTEM DEFECTIVE CHAIN: A;	DNA-BINDING PROTEIN HELIX-TURN-HELIX, DNA-BINDING PROTEIN
1508	1san		22	80	5.1e-29	0.78	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1508	9ant	A	20	75	3.4e-29	0.39	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1526	1a8p		70	306	1.8e-29	0.31	1.00		NADPH\;FERREDOXIN OXIDOREDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FERREDOXIN REDUCTASE; OXIDOREDUCTASE
1526	1a8p		75	315	1.8e-29			66.86	NADPH\;FERREDOXIN OXIDOREDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FERREDOXIN REDUCTASE; OXIDOREDUCTASE
1526	1cqx	A	46	314	8.5e-41	0.29	0.98		FLAVOHEMOPROTEIN; CHAIN: A, B	LIPID BINDING PROTEIN GLOBIN FOLD, SIX- STRANDED ANTIPARALLEL BETA SHEET; HELIX- 2 FLANKED FIVE-STRANDED PARALLEL BETA SHEET, LIPID BINDING 3 PROTEIN
1526	1ddg	A	86	309	1.4e-26	-0.18	0.13		SULFITE REDUCTASE (NADPH) FLAVOPROTEIN ALPHA- CHAIN: A, B;	OXIDOREDUCTASE CYTOCHROME P450 REDUCTASE, FNR, FLAVOPROTEIN, MODULAR 2 PROTEIN, OXIDOREDUCTASE
1526	1fdr		75	313	1.4e-31			66.92	FLAVODOXIN REDUCTASE; CHAIN: NULL;	FLAVOPROTEIN FERREDOXIN REDUCTASE; FLAVODOXIN REDUCTASE, FERREDOXIN REDUCTASE, FLAVIN, 2 OXIDOREDUCTASE, FLAVOPROTEIN
1526	1fdr		82	303	1.4e-31	0.44	0.84		FLAVODOXIN REDUCTASE; CHAIN: NULL;	FLAVOPROTEIN FERREDOXIN REDUCTASE; FLAVODOXIN REDUCTASE, FERREDOXIN REDUCTASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FLAVIN, 2 OXIDOREDUCTASE, FLAVOPROTEIN
1526	1fmb		59	314	1.6e-21			62.28	OXIDOREDUCTASE (NADP+(A), FERREDOXIN(A)) FERREDOXIN:NADP+ OXIDOREDUCTASE (FERREDOXIN REDUCTASE, 1FNB 3 FLAVOENZYME) (E.C.1.18.1.2) 1FNB 4 1FNB 72	
1526	1ndh		69	315	1.7e-70			124.42	ELECTRON TRANSPORT (FLAVO PROTEIN) CYTOCHROME B-5= REDUCTASE (E.C.1.6.2.2) 1NDH 3	
1526	1ndh		70	315	1.7e-70	0.44	1.00		ELECTRON TRANSPORT (FLAVO PROTEIN) CYTOCHROME B-5= REDUCTASE (E.C.1.6.2.2) 1NDH 3	
1526	1qff	A	76	315	1e-33			71.47	FLAVIN REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1526	1qff	A	80	313	3.4e-26	0.34	1.00		FLAVIN REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1526	1qff	A	82	303	1e-33	0.50	0.92		FLAVIN REDUCTASE; CHAIN: A,	OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, D;	RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1526	1qfz	A	47	314	2e-29			66.01	FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE FNR; FLAVOENZYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDRIDE 2 TRANSFER, OXIDOREDUCTASE
1526	1qfz	A	72	310	2e-29	0.06	0.80		FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE FNR; FLAVOENZYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDRIDE 2 TRANSFER, OXIDOREDUCTASE
1526	1que		59	313	6e-31			54.28	FERREDOXIN--NADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1526	1que		69	310	6e-31	0.35	0.47		FERREDOXIN--NADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1526	2cnd		76	315	8.5e-68			111.11	OXIDOREDUCTASE (NITROGENOUS ACCEPTOR) NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT) (E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	
1526	2cnd		78	314	8.5e-68	0.96	1.00		OXIDOREDUCTASE (NITROGENOUS ACCEPTOR) NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT) (E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	
1532	1alh	A	267	344	1.7e-27	-0.00	0.19		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1532	1alh	A	290	373	5.1e-28	-0.23	0.57		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1532	1d0s	A	631	970	1.2e-19	0.17	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN:	TRANSFERASE DINUCLEOTIDE-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									A;	MOTIF, PHOSPHORIBOSYL TRANSFERASE
1532	1mey	C	266	342	1e-46	-0.08	0.41		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1532	1mey	C	289	373	6.8e-47	-0.08	0.76		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1532	1mey	G	402	432	8.5e-10	0.31	0.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1532	1ff6	A	213	362	3.4e-31	-0.22	0.52		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1532	1ff6	A	239	428	1.7e-33	-0.02	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1532	1ubd	C	241	342	2.4e-14	-0.16	0.52		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1532	1ubd	C	274	373	1.4e-28	0.17	0.83		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1532	2adr		405	462	5.1e-08	0.01	-0.17		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1533	1av1	A	210	405	0.00034			69.97	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1533	1cun	A	211	425	0.00036			61.27	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1533	1quu	A	168	416	7.2e-08			60.38	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1534	1awc	B	329	476	3.4e-29	0.02	-0.15		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1534	1awc	B	405	540	1.7e-30	0.18	-0.15		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPALPHA; GABBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1534	1btm		508	608	4.8e-19	0.12	0.07		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
1534	1btm		90	177	2.4e-07	0.33	0.99		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
1534	1dro		107	181	0.00048	0.19	0.13		BETA-SPECTRIN; 1DRO 6 CHAIN: NULL; 1DRO 7	CYTOSKELETON
1534	1fgy	A	90	177	3.6e-13	0.42	0.53		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1534	1pbw	A	720	895	4.8e-45	0.61	1.00		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1534	1pbw	B	720	899	1.1e-44	0.46	0.99		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1534	1pms		1057	1151	1.1e-08	0.29	0.51		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1534	1pms		88	178	2.4e-10	0.10	0.39		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1534	1x4	A	718	899	6e-46	0.46	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1535	1bd8		289	444	3.4e-18	0.04	-0.19		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1535	1bi7	B	360	476	3.4e-18	0.02	0.05		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1535	1btm		90	177	2.4e-07	0.33	0.99		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
1535	1d9s	A	369	481	1e-18	0.21	-0.13		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1535	1dro		107	181	0.00048	0.19	0.13		BETA-SPECTRIN; 1DRO 6 CHAIN: NULL; 1DRO 7	CYTOSKELETON
1535	1fgy	A	1058	1136	4.8e-05	0.42	0.87		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1535	1fgy	A	90	177	3.6e-13	0.42	0.53		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1535	1ihb	A	286	445	1.7e-20	0.14	-0.14		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1535	1pbw	A	720	895	4.8e-45	0.61	1.00		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1535	1pbw	B	720	899	1.1e-44	0.46	0.99		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1535	1pms		1057	1140	1.2e-06	0.16	0.39		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1535	1pms		88	178	2.4e-10	0.10	0.39		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1535	1rx4	A	718	899	6e-46	0.46	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										(GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1536	1bu1	A	30	73	3.4e-11	-0.56	0.07		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1536	1cka	A	28	72	5.1e-12	-0.81	0.45		COMPLEX (ONCOGENE PROTEIN/PEPTIDE) C-CRK (N-TERMINAL SH3 DOMAIN) (C-CRKSH3-N) COMPLEXED WITH 1CKA 3 C3G PEPTIDE (PRO-PRO-PRO-ALA-LEU-PRO-PRO-LYS-LYS-ARG) 1CKA 4	
1536	1efn	A	28	71	8.5e-15	-0.15	0.40		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1536	1fmk		27	79	3.4e-15	-0.59	0.34		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PXXP MOTIF PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1536	1fyn	A	27	73	1.2e-15	-0.20	0.18		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1536	1nlo	C	136	187	5.1e-09	0.13	-0.19		C-SRC; CHAIN: C; NLI (MN7-MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1536	1nlo	C	27	71	1e-14	-0.33	0.80		C-SRC; CHAIN: C; NLI (MN7-MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1536	1sem	A	31	69	1e-12	-0.64	0.43		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
1536	1shf	A	27	73	1.2e-15	-0.19	0.12		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1536	4hck		30	73	3.4e-11	-0.47	0.09		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1546	1a17		134	248	1.5e-22	-0.11	1.00		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1546	1a17		16	154	1.4e-23	-0.06	0.35		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1546	1a17		87	224	1.3e-07	0.25	0.68		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1546	1e96	B	101	249	3.4e-12	0.15	0.89		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1546	1e96	B	17	166	3.4e-14	0.08	0.15		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1546	1e1r	A	133	250	6.8e-18	0.11	1.00		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE- COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1546	1e1r	A	16	140	1.4e-16	0.08	-0.13		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE- COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1546	1e1r	A	3	90	8.5e-14	0.03	-0.19		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	CHAPERONE HOP, TPR- DOMAIN, PEPTIDE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									MEEVD; CHAIN: B;	COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1546	1elr	A	66	166	3.4e-17	0.10	0.25		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1546	1elw	A	132	249	3.4e-20	0.09	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1546	1elw	A	16	132	1.5e-17	0.07	0.17		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1546	1elw	A	67	174	1.7e-13	0.34	0.25		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1546	1elw	A	96	194	2.6e-07	0.02	0.37		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1546	1fch	A	7	251	6.8e-31	0.17	0.99		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: C, D;	PROTEIN-PEPTIDE COMPLEX, TETRATRIPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1546	1qqe	A	109	239	5.1e-05	-0.38	0.05		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1546	1qqe	A	13	194	1.4e-10	0.25	0.07		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1546	1qqe	A	2	253	1.4e-10			56.33	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1556	1a06		1	300	3.4e-81			72.75	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1556	1a06		1	300	3.4e-81			72.75	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1556	1a06		6	286	3.4e-81	0.02	0.82		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1556	1a06		6	286	3.4e-81	0.02	0.82		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1556	1a60		3	311	1.5e-42			78.86	PROTEIN KINASE CK2/ALPHA-	TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SUBUNIT; CHAIN: NULL;	TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1556	1a60		3	311	1.5e-42			78.86	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1556	1apm	E	1	319	0			97.24	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1556	1apm	E	1	319	0			97.24	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1556	1apm	E	5	284	0	0.32	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1556	1apm	E	5	284	0	0.32	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1556	1aq1		5	271	8.5e-56	0.24	0.99		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1556	1aq1		5	271	8.5e-56	0.24	0.99		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1556	1aq1		5	314	8.5e-56			81.86	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1556	1aq1		5	314	8.5e-56			81.86	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1556	1bi8	A	6	303	1.4e-45			84.40	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1556	1bi8	A	6	303	1.4e-45			84.40	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-	COMPLEX (KINASE/INHIBITOR) CDK6;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1556	1blx	A	1	311	1e-49			96.61	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1556	1blx	A	1	311	1e-49			96.61	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1556	1byg	A	1	278	1.7e-35			74.25	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1556	1byg	A	1	278	1.7e-35			74.25	C-TERMINAL SRC KINASE;	TRANSFERASE CSK;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A;	PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1556	1cmk	E	1	319	0			94.17	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1556	1cmk	E	1	319	0			94.17	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1556	1cmk	E	4	284	0	0.28	1.00		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1556	1cmk	E	4	284	0	0.28	1.00		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1556	1ctp	E	1	306	0			94.73	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1556	1ctp	E	1	306	0			94.73	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1556	1ctp	E	4	292	0	0.32	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1556	1ctp	E	4	292	0	0.32	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1556	1f3m	C	7	286	5.1e-81	0.14	0.98		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1556	1f3m	C	7	286	5.1e-81	0.14	0.98		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1556	1fgk	A	1	273	1.7e-37			86.10	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1556	1fgk	A	1	273	1.7e-37			86.10	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1556	1fgk	B	1	272	1.4e-39			71.13	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1556	1fgk	B	1	272	1.4e-39			71.13	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1556	1hcl		5	271	5.1e-59	0.38	0.99		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1556	1hcl		5	271	5.1e-59	0.38	0.99		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1556	1hcl		5	314	5.1e-59			101.86	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1556	1hcl		5	314	5.1e-59			101.86	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1556	1ian		1	325	3.4e-42			78.76	P38 MAP KINASE; CHAIN: NULL;	PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1556	lian		1	325	3.4e-42			78.76	P38 MAP KINASE; CHAIN: NULL;	PROTEIN KINASE SERINE/THREONINE- PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR- KINASE, SERINE/THREONINE- PROTEIN KINASE
1556	lir3	A	1	289	1.2e-34			82.74	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1556	lir3	A	1	289	1.2e-34			82.74	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1556	ljnk		3	340	6.8e-46			89.07	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1556	1jnk		3	340	6.8e-46			89.07	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	PROTEIN 2 KINASE TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1556	1koa		5	287	6.8e-68	0.36	0.99		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1556	1koa		5	287	6.8e-68	0.36	0.99		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1556	1kob	A	1	326	3.4e-67			95.11	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1556	1kob	A	1	326	3.4e-67			95.11	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1556	1kob	A	6	267	3.4e-67	0.13	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1556	1kob	A	6	267	3.4e-67	0.13	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1556	1p38		1	327	5.1e-48			98.98	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE- PROTEIN KINASE, 2 P38
1556	1p38		1	327	5.1e-48			98.98	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE- PROTEIN KINASE, 2 P38
1556	1phk		5	269	5.1e-78			106.76	PHOSPHORYLASE KINASE;	KINASE RABBIT MUSCLE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: NULL;	PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP- BINDING, CALMODULIN- BINDING
1556	1phk		5	269	5.1e-78			106.76	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP- BINDING, CALMODULIN- BINDING
1556	1phk		6	266	5.1e-78	0.44	1.00		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP- BINDING, CALMODULIN- BINDING
1556	1phk		6	266	5.1e-78	0.44	1.00		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP- BINDING, CALMODULIN- BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1556	1pme		1	319	3.4e-44			88.01	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1556	1pme		1	319	3.4e-44			88.01	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1556	1tki	A	2	323	3.4e-54			91.81	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1556	1tki	A	2	323	3.4e-54			91.81	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1556	3erk		1	324	3.4e-47			90.63	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1556	3erk		1	324	3.4e-47			90.63	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1557	1a06		1	303	1.7e-83			81.40	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1557	1a06		1	303	1.7e-83			81.40	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1557	1a06		8	270	1.7e-83	0.15	1.00		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1557	1a06		8	270	1.7e-83	0.15	1.00		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1557	1a60		3	311	6.8e-43			80.48	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE- PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1557	1a60		3	311	6.8e-43			80.48	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE- PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1557	1apm	E	1	319	0			104.15	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									AND THE DETERGENT MEGA-8 1APM 6	
1557	1apm	E	1	319	0			104.15	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1557	1apm	E	5	265	0	0.54	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1557	1apm	E	5	265	0	0.54	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1557	1aq1		5	277	1.7e-52			88.38	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1557	1aq1		5	277	1.7e-52			88.38	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1557	1b6c	B	1	301	1.2e-24			71.44	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1557	1b6c	B	1	301	1.2e-24			71.44	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									I; CHAIN: B, D, F, H;	SERINE/THREONINE- PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1557	1bi8	A	6	303	5.1e-43			89.80	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1557	1bi8	A	6	303	5.1e-43			89.80	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1557	1blx	A	1	311	1.4e-46			102.80	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1557	1blx	A	1	311	1.4e-46			102.80	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1557	1byg	A	1	277	3.4e-31			84.49	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1557	1byg	A	1	277	3.4e-31			84.49	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1557	1cmk	E	1	319	0			101.22	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1557	1cmk	E	1	319	0			101.22	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1557	1cmk	E	5	265	0	0.45	1.00		(E.C.2.7.1.37) 1CMK 4 PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1557	1cmk	E	5	265	0	0.45	1.00		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1557	1ctp	E	1	316	0			103.71	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1557	1ctp	E	1	316	0			103.71	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1557	1ctp	E	5	265	0	0.34	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1557	1ctp	E	5	265	0	0.34	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1557	1f3m	C	7	270	8.5e-56	-0.09	1.00		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A ₃	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	FRAGMENT, HOMODIMER
1557	1f3m	C	7	270	8.5e-56	-0.09	1.00		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1557	1fgk	A	1	273	1.4e-33			95.46	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1557	1fgk	A	1	273	1.4e-33			95.46	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1557	1fgk	B	1	272	6.8e-35			79.45	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1557	1fgk	B	1	272	6.8e-35			79.45	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1557	1hcl		5	269	5.1e-55	0.56	1.00		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1557	1hcl		5	269	5.1e-55	0.56	1.00		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1557	1hcl		5	302	5.1e-55			107.22	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1557	1hcl		5	302	5.1e-55			107.22	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1557	1ian		1	325	1.7e-40			82.78	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1557	1ian		1	325	1.7e-40			82.78	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1557	1ir3	A	1	289	4.8e-30			93.03	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1557	1ir3	A	1	289	4.8e-30			93.03	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1557	1jnk		3	341	8.5e-44			91.74	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1557	1jnk		3	341	8.5e-44			91.74	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1557	1koa		5	270	1.7e-68	0.19	0.99		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1557	1koa		5	270	1.7e-68	0.19	0.99		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1557	1kob	A	1	326	8.5e-68			106.72	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1557	1kob	A	1	326	8.5e-68			106.72	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1557	1kob	A	6	268	8.5e-68	0.20	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1557	1kob	A	6	268	8.5e-68	0.20	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1557	1p38		1	327	1.7e-46			105.39	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1557	1p38		1	327	1.7e-46			105.39	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1557	1phk		5	269	1.7e-80			116.22	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1557	1phk		5	269	1.7e-80			116.22	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1557	1phk		6	269	1.7e-80	0.50	1.00		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1557	1phk		6	269	1.7e-80	0.50	1.00		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1557	1pme		1	350	6.8e-43			97.20	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1557	1pme		1	350	6.8e-43			97.20	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1557	1quu	A	239	347	4.8e-05	0.22	0.05		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										COIL, CONTRACTILE PROTEIN
1557	1quu	A	239	347	4.8e-05	0.22	0.05		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1557	1tki	A	2	323	1e-54			101.04	TITIN; CHAIN: A; B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1557	1tki	A	2	323	1e-54			101.04	TITIN; CHAIN: A; B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1557	1tki	A	6	266	1e-54	0.33	1.00		TITIN; CHAIN: A; B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1557	1tki	A	6	266	1e-54	0.33	1.00		TITIN; CHAIN: A; B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1557	3erk		1	348	3.4e-44			100.10	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1557	3erk		1	348	3.4e-44			100.10	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										KINASE, 2 ERK2
1563	1bkd		S1153	1549	2.4e-96			196.51	H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1563	1bkd		S1209	1548	2.4e-96	0.06	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1563	1bkd		S946	1001	3.6e-15	-0.28	0.05		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1563	1btk	A	333	444	6e-05	0.43	0.47		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
1563	1btk		329	443	1.1e-08	0.53	0.45		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
1563	1f5x	A	548	722	2.4e-37	0.15	0.96		RHO-GEF VAV; CHAIN: A;	SIGNALING PROTEIN 11 ALPHA-HELICES
1563	1fgy	A	337	447	9.6e-16	0.83	0.59		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1563	1pms		313	445	2.4e-12	0.19	-0.15		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1564	1bkd		S634	689	3.6e-15	-0.28	0.05		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1564	1bkd		S841	1237	2.4e-96			197.78	H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1564	1bkd		S897	1236	2.4e-96	0.06	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1564	1bkd		S994	1235	5.1e-20	0.40	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
1564	1btk	A	21	132	6e-05	0.43	0.47		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
1564	1bmn		17	131	1.1e-08	0.53	0.45		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
1564	1f5x	A	236	410	2.4e-37	0.15	0.96		RHO-GEF VAV; CHAIN: A;	SIGNALING PROTEIN 11 ALPHA-HELICES
1564	1fgy	A	25	135	9.6e-16	0.83	0.59		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1570	1aut	L	178	266	5.1e-11	0.14	-0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1570	1ckl	A	220	276	6e-14	1.17	0.82		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										MEASLES VIRUS, GLYCOPROTEIN
1570	1ckl	A	220	302	2.4e-12	0.53	0.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1570	1ckl	A	48	103	9.6e-13	0.54	0.81		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1570	1e5g	A	220	346	1.2e-11	0.58	0.19		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
1570	1e5g	A	48	158	1.2e-13	0.20	-0.15		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
1570	1emm		216	289	6.8e-12	0.05	-0.15		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1570	1hcc		216	275	3.6e-14	0.97	0.65		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H 1HCC 3	
1570	1hcc		47	104	1.2e-13	0.22	0.19		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H 1HCC 3	
1570	1klo		51	224	1.7e-12	0.03	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1570	1qub	A	180	394	1.4e-14	0.13	-0.18		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1570	1qub	A	46	361	3.4e-23			97.15	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1570	1qub	A	47	282	3.4e-23	0.08	-0.03		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	DOMAIN, MEMBRANE ADHESION
1570	1sfp		105	212	6e-27	0.81	0.76		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1570	1sfp		272	394	1.2e-21	0.73	0.88		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1570	1spp	A	107	214	4.8e-27	0.89	0.35		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									GLYCOPROTEIN PSP-II; CHAIN: B	PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)
1570	1spp	A	279	385	3.6e-21	0.71	0.94		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)
1570	1vvc		219	305	2.4e-16	1.00	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
1570	1vvc		48	134	3.6e-16	0.23	0.92		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
1570	1vvc		7	102	5.1e-09	-0.02	0.06		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1571	1buo	A	76	203	3.4e-18	0.30	0.60		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1571	1gof		411	466	1.7e-07	-0.50	0.10		OXIDOREDUCTASE(OXYGEN(A) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
1572	1d0s	A	279	621	2.4e-12	0.23	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1577	1dcq	A	10	131	1.7e-17	0.12	0.72		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1577	1dkx	A	228	310	0.0024	0.02	0.11		SUBSTRATE BINDING DOMAIN OF DNAK; CHAIN: A; SUBSTRATE PEPTIDE (7 RESIDUES); CHAIN: B;	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE) DNAK, HEAT SHOCK PROTEIN 70 KDA (HSP70), COMPLEX 2 (MOLECULAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CHAPERONE/PEPTIDE)
1579	1quu	A	172	388	1.2e-08	-0.13	0.09		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1579	1quu	A	94	340	1.2e-08			51.99	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1582	1aut	L	27	127	3.6e-10	0.22	-0.11		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1582	1aut	L	56	152	3.6e-10			51.62	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1582	1dx5	I	31	151	1.2e-09	0.09	-0.18		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN	SERINE PROTEINASE COAGULATION FACTOR II;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1582	1eis	A	26	105	9.6e-09	0.45	0.41		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1582	1eis	A	4	56	6e-06	-0.46	0.68		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1582	1ext	A	11	154	3.6e-13			52.32	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1582	1ext	A	4	143	3.6e-13	0.00	-0.12		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1582	1pfx	L	19	147	8.4e-17			52.22	FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1584	1d2h	A	137	249	3.4e-16	-0.13	0.16		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1587	1xbr	A	1	143	3.4e-51	-0.11	1.00		T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-BINDING PROTEIN
1587	1xbr	A	1	150	6e-61	0.09	1.00		T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-BINDING PROTEIN
1587	1xbr	A	1	153	6e-61			96.33	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-BINDING PROTEIN
1591	1b37	A	51	86	8.5e-07	-0.01	0.31		POLYAMINE OXIDASE; CHAIN: A, B, C;	OXIDOREDUCTASE FLAVIN-DEPENDENT AMINE OXIDASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1591	1c0p	A	232	262	1.7e-05	-0.57	0.12		D-AMINO ACID OXIDASE; CHAIN: A;	OXIDOREDUCTASE
1591	1djn	A	37	426	1.5e-13	-0.39	0.04		TRIMETHYLAMINE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE ALPHA-BETA-ALPHA MOTIF, FLAVIN CONTAINING PROTEIN, OXIDASE
1591	1ebd	A	53	525	0	-0.29	0.05		DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B; DIHYDROLIPOAMIDE ACETYLTRANSFERASE; CHAIN: C;	OXIDOREDUCTASE IRON-SULFUR FLAVOPROTEIN, ELECTRON TRANSFER, OXIDOREDUCTASE
1591	1f8s	A	49	150	1.2e-10	-0.46	0.00		L-AMINO ACID OXIDASE; CHAIN: A, B, C, D, E, F, G, H;	COMPLEX (OXIDOREDUCTASE/TRANSFERASE) E3BD; REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE
1591	1lpf	A	49	523	0	-0.28	0.42		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LPF 3 FLAVIN-ADENINE-DINUCLEOTIDE (FAD) 1LPF 4	OXIDOREDUCTASE FLAVOENZYME, OXIDASE, ENANTIOMERIC SPECIFICITY, O-2 AMINOBENZOATE, ACTIVE SITE FUNNEL, HELICAL DOMAIN, FAD- 3 BINDING DOMAIN
1591	1nhp		87	551	5.1e-59			66.44	OXIDOREDUCTASE (H2O2(A)) NADH PEROXIDASE (NPX)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1591	1ojt		45	535	3.4e-95	-0.28	0.11		(E.C.1.11.1.1) MUTANT WITH CYS 42 INHP 3 REPLACED BY ALA (C42A) INHP 4	
1591	1ojt		45	540	3.4e-95				SURFACE PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 FLAVOPROTEIN, FAD, P64K
1591	1pbe		48	80	0.00034	-0.25	0.41		OXIDOREDUCTASE P-HYDROXYBENZOATE HYDROXYLASE (PHBH) (E.C.1.14.13.2) 1PBE 3 COMPLEXED WITH P-HYDROXYBENZOIC ACID 1PBE 4	OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 FLAVOPROTEIN, FAD, P64K
1591	1trb		47	402	5.1e-59	-0.24	0.51		OXIDOREDUCTASE(FLAVOENZ YME) THIOREDOXIN REDUCTASE (E.C.1.6.4.5) MUTANT WITH CYS 138 1TRB 3 REPLACED BY SER (C138S) 1TRB 4	
1591	1vdc		47	402	1.7e-53	-0.44	0.12		NADPH DEPENDENT THIOREDOXIN REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE NTR; HYPOTHETICAL PROTEIN, REDOX-ACTIVE CENTER, OXIDOREDUCTASE, 2 DISULFIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										OXIDOREDUCTASE, THIOREDOXIN REDUCTASE, FLAVIN 3 ADENINE DINUCLEOTIDE
1591	3hdh	A	50	84	0.0014	-0.11	0.01		L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
1591	3hdh	A	50	84	0.0014	-0.11	0.01		L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
1591	3hdh	C	50	84	0.0014	-0.41	0.00		L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
1591	3hdh	C	50	86	0.00014	-0.20	0.25		L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										+ NADH
1591	3lad	A	49	523	6.8e-100	-0.36	0.33		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	
1592	1aog	A	86	563	8.5e-76	-0.22	0.12		TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE TRYPANOTHIONE REDUCTASE, FAD DEPENDENT DISULPHIDE 2 OXIDOREDUCTASE
1592	1c0p	A	270	300	6.8e-05	-0.57	0.12		D-AMINO ACID OXIDASE; CHAIN: A;	OXIDOREDUCTASE ALPHA- BETA-ALPHA MOTIF, FLAVIN CONTAINING PROTEIN, OXIDASE
1592	1chu	A	84	414	1.5e-09	0.16	0.18		L-ASPARTATE OXIDASE; CHAIN: A;	FLAVOENZYME FLAVOENZYME, NAD BIOSYNTHESIS, FAD, OXIDOREDUCTASE
1592	1f8s	A	87	188	1.2e-10	-0.46	0.00		L-AMINO ACID OXIDASE; CHAIN: A, B, C, D, E, F, G, H;	OXIDOREDUCTASE FLAVOENZYME, OXIDASE, ENANTIOMERIC SPECIFICITY, O-2 AMINO BENZOATE, ACTIVE SITE FUNNEL, HELICAL DOMAIN, FAD-3 BINDING DOMAIN
1592	1f8s	A	88	135	5.1e-09	-0.13	0.23		L-AMINO ACID OXIDASE; CHAIN: A, B, C, D, E, F, G, H;	OXIDOREDUCTASE FLAVOENZYME, OXIDASE, ENANTIOMERIC SPECIFICITY, O-2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1592	1lpf	A	87	561	0	-0.14	0.11		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LPF 3 FLAVIN-ADENINE-DINUCLEOTIDE (FAD) 1LPF 4	AMINOBENZOATE, ACTIVE SITE FUNNEL, HELICAL DOMAIN, FAD- 3 BINDING DOMAIN
1592	1nhp		125	589	1.7e-61			67.46	OXIDOREDUCTASE (H2O2(A)) NADH PEROXIDASE (NPX) (E.C.1.11.1.1) MUTANT WITH CYS 42 INHP 3 REPLACED BY ALA (C42A) 1NHP 4	
1592	1ojt		83	578	1.5e-96			68.88	SURFACE PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 FLAVOPROTEIN, FAD, P64K
1592	1trb		85	440	8.5e-63	-0.09	0.30		OXIDOREDUCTASE(FLAVOENZ YME) THIOREDOXIN REDUCTASE (E.C.1.6.4.5) MUTANT WITH CYS 138 1TRB 3 REPLACED BY SER (C138S) 1TRB 4	
1592	3lad	A	87	561	3.4e-98	-0.29	0.05		OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1594	1a7i		25	86	1.7e-07	-0.24	0.31		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1594	1a7i		27	86	2.2e-18	0.14	0.49		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1594	1a7i		88	146	8.8e-11	0.19	0.75		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1594	1ahd	P	191	256	1.7e-27	-0.25	0.09		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1594	1b72	A	195	250	3.4e-24	0.58	0.40		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1594	1b8i	A	195	249	1e-23	0.21	0.71		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'-	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: D;	DEVELOPMENT, 2 SPECIFICITY
1594	1b8t	A	24	149	3.4e-10	-0.10	0.04		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1594	1b8t	A	27	98	1.7e-11	-0.19	0.21		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1594	1b8t	A	85	279	3.4e-09			55.32	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1594	1b8t	A	86	228	3.4e-09	-0.55	0.23		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1594	1bw5		189	254	3.4e-17			89.50	INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1594	1ctl		17	105	2e-16			51.64	AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1594	1ctl		19	81	2e-16	0.09	0.98		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1594	1ctl		27	98	1.7e-11	-0.23	0.17		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1594	1ctl		88	143	1.8e-10	0.10	0.53		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1594	1ctl		89	149	5.1e-05	-0.13	0.34		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1594	1cxx	A	24	81	5.1e-09	0.18	0.65		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1594	1cxx	A	27	83	2e-15	0.16	0.46		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1594	1cxx	A	86	145	0.0001	0.53	0.99		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1594	1cxx	A	88	143	1.3e-10	-0.18	1.00		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1594	1enh		193	245	8.5e-18	0.21	0.84		DNA-BINDING PROTEIN ENGRAILED HOMEODOMAIN 1ENH 3	
1594	1fjl	A	190	250	3.4e-22	0.03	0.68		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1594	1fj	B	191	248	3.4e-21	0.08	0.55		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1594	1ftz		190	256	3.4e-24	-0.04	0.12		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1594	1iml		25	91	1.4e-08	-0.21	0.33		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1594	1iml		27	99	2.2e-21	-0.13	0.60		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1594	1iml		87	161	0.00017	0.27	0.42		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1594	1iml		88	142	2.2e-10	0.01	0.76		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1594	1san		197	256	1.7e-25	0.27	0.24		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4	

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1594	2hdd	B	192	247	1.2e-17	0.34	0.72		(NMR, 20 STRUCTURES) ISAN 5 ENGRAILED HOMEODOMAIN; CHAIN: A, B; DNA (20-MER); CHAIN: C, D;	COMPLEX (DNA BINDING PROTEIN/DNA) DNA BINDING, COMPLEX (DNA BINDING PROTEIN/DNA)
1594	9ant	A	195	250	1.4e-25	0.19	0.34		ANTENNAPEPIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1621	1a4y	A	158	354	3.4e-32	0.30	0.94		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1621	1a4y	A	168	414	1.2e-48	0.28	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1621	1a4y	A	37	330	3.6e-23	0.32	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN;	COMPLEX (INHIBITOR/NUCLEASE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1621	1a4y	A	40	427	6e-19	0.44	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1621	1d0b	A	237	398	8.5e-07	0.13	0.28		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1621	1dce	A	170	278	8.5e-05	0.02	0.06		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1621	1f6l	B	168	303	5.1e-05	0.46	0.09		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1621	1fqv	A	36	110	0.0096	0.46	0.63		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LEUCINE-RICH-REPEAT 2 (LRR) LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1621	1fqv	A	40	288	9.6e-07	0.20	0.90		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1621	1yrg	A	157	408	1.5e-12	0.38	0.35		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE
1621	2bnh		168	414	1.7e-52	0.15	0.98		RIBONUCLEASE INHIBITOR;	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: NULL;	INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1621	2bnh		23	113	0.0012	0.12	0.40		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1621	2bnh		66	339	1.2e-33	0.45	0.98		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1623	1crz	A	107	218	0.00051	0.08	0.90		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1623	1crz	A	111	243	6e-07	0.13	0.66		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1623	1crz	A	564	764	5.1e-05	0.49	0.15		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1623	1crz	A	674	876	6.8e-05	-0.08	0.04		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1623	1erj	A	1012	1291	1.5e-60	0.09	-0.20		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	153	646	2e-17	0.11	0.24		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	190	523	3.4e-60	0.31	0.24		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	2	224	1.2e-47	0.42	0.84		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	251	562	3.4e-57	0.43	-0.09		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	31	344	3.4e-58	0.41	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	339	650	3.4e-58	0.23	-0.06		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	364	813	6e-31	0.33	0.31		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	572	856	1e-61	0.28	0.59		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	666	949	1e-61	0.20	-0.11		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1erj	A	700	994	5.1e-58	0.04	-0.15		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1623	1got	B	105	441	3.4e-54	0.52	0.83		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	239	559	6.8e-56	0.30	0.10		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	299	695	1.4e-19	0.10	0.75		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	3	282	5.1e-69	0.36	0.74		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	345	648	1.4e-49	0.24	0.40		GT-ALPHA/GI-ALPHA CHIMERA;	COMPLEX (GTP-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	398	695	6.8e-51	0.12	0.34		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	494	813	8e-23	0.38	0.05		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	563	853	8.5e-70	0.41	0.49		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	60	387	1.7e-61	0.50	0.71		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	655	950	3.4e-60	0.15	-0.15		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1623	1got	B	745	1041	1.7e-65	0.06	-0.18		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1624	1b91	A	42	153	1.7e-27	0.40	1.00		HISTONE ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE BROMODOMAIN, HISTONE-ACETYLTRANSFERASE, NMR-STRUCTURE
1624	1e6i	A	54	154	3.4e-29	0.03	0.96		TRANSCRIPTIONAL ACTIVATOR GCN5; CHAIN: A; H4 PEPTIDE; CHAIN: P;	GENE REGULATION BROMODOMAIN, HISTONE BINDING, N-ACETYL LYSINE
1624	1eqf	A	24	151	1e-22	0.01	0.51		RNA POLYMERASE II TRANSCRIPTION INITIATION CHAIN: A;	TRANSCRIPTION TAFII250; FOUR-HELIX BUNDLE, ACETYLATED HISTONE-TAIL BINDING PROTEIN
1624	1eqf	A	58	239	2e-20	-0.26	0.90		RNA POLYMERASE II TRANSCRIPTION INITIATION CHAIN: A;	TRANSCRIPTION TAFII250; FOUR-HELIX BUNDLE, ACETYLATED HISTONE-TAIL BINDING PROTEIN
1631	1alh	A	140	199	5.1e-17	0.20	0.49		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1631	1alh	A	148	227	1.2e-26	0.29	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1631	1alh	A	175	256	8e-36	0.29	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SITE; CHAIN: B, C;	FINGER, DNA-BINDING PROTEIN
1631	1alh	A	204	284	2e-36	0.27	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1631	1alh	A	315	396	1.4e-35	0.17	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1631	1alh	A	315	397	1.4e-35			77.27	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1631	1b8t	A	141	337	8e-14			59.99	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1631	1mey	C	142	199	8.5e-29	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	146	227	1.4e-46	0.40	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	174	255	6.8e-50	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	174	256	1.7e-51			98.68	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	202	283	1.7e-51	0.31	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	230	311	5.1e-51	0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ I'OLD score	Compound	PDB annotation
1631	1mey	C	258	367	1.4e-46	-0.26	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	314	395	1.7e-38	0.06	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	C	342	426	8.5e-49	0.06	0.74		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1mey	G	144	171	5.1e-09	0.70	0.43		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1631	1tf3	A	143	195	5.1e-11	0.34	0.07		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: E, F;	5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1631	1tf3	A	147	227	6.8e-20	0.47	0.90		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1631	1tf6	A	146	314	4e-59			108.16	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1tf6	A	147	292	1.5e-37	0.08	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1tf6	A	153	283	4e-42	-0.10	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1tf6	A	175	339	4e-58	-0.11	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1tf6	A	204	367	4e-59	-0.21	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1tf6	A	231	395	8e-59	-0.14	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1ff6	A	259	409	8.5e-34	-0.28	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1ff6	A	287	453	1.4e-31	-0.28	0.35		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1631	1ubd	C	141	227	1.2e-28	0.24	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	149	256	1.8e-43			85.96	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	151	255	8e-36	0.11	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	154	255	1e-33	0.10	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	178	283	1.8e-43	0.36	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	210	311	1.5e-35	0.14	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	228	340	8e-46	0.09	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	266	395	1.2e-30	-0.24	0.71		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	1ubd	C	284	395	8e-45	-0.06	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1631	2gli	A	151	285	4e-38	0.07	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1631	2gli	A	154	282	1e-34	-0.02	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1631	2gli	A	175	313	8e-57	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1631	2gli	A	200	341	4e-59			92.55	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1631	2gli	A	202	369	4e-59	0.13	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1631	2gli	A	258	396	1e-57	0.14	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1631	2gli	A	294	455	3.4e-32	-0.15	0.19		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1644	1osm	A	18	212	2.2e-08	0.84	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1644	1req	A	487	581	2.2e-10	0.22	-0.18		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
1645	1ahd	P	100	166	1.7e-27	0.38	0.13		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1645	1ahd	P	16	75	6.8e-31	0.29	0.52		STRUCTURES) 1AHD 5 DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1645	1b72	A	105	161	5.1e-22	0.60	0.86		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1645	1b72	A	19	75	5.1e-25	0.17	0.77		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1645	1b8i	A	105	159	3.4e-24	0.37	0.65		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1645	1b8i	A	19	73	3.4e-27	0.35	0.84		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1645	1du0	B	103	158	1e-14	0.35	0.75		ENGRAILED HOMEODOMAIN;	TRANSCRIPTION/DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	HOMEOTIC PROTEIN ENGRAILED, SEGMENTATION POLARITY HOMEODOMAIN, DNA-BINDING PROTEIN, PROTEIN-DNA COMPLEX
1645	1enh		103	155	6.8e-15	0.39	0.95		DNA-BINDING PROTEIN ENGRAILED HOMEODOMAIN 1ENH 3	
1645	1enh		17	69	3.4e-19	0.63	0.99		DNA-BINDING PROTEIN ENGRAILED HOMEODOMAIN 1ENH 3	
1645	1fjl	A	102	160	3.4e-20	0.28	0.92		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1645	1fjl	A	14	74	3.4e-25	0.15	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1645	1fjl	B	102	158	3.4e-19	0.31	0.88		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1645	1fjl	B	15	72	1.4e-23	0.35	1.00		PAIRED PROTEIN; CHAIN: A, B,	COMPLEX (DNA-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									C; DNA; CHAIN: D, E, F	PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1645	1ftz		15	82	8.5e-27	0.15	0.46		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1645	1ftz		99	166	3.4e-23	-0.15	0.01		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1645	1san		107	166	5.1e-26	0.21	0.72		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1645	1san		21	75	1.5e-28	0.50	0.78		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1645	2hdd	B	16	71	3.4e-19	0.25	0.92		ENGRAILED HOMEODOMAIN; CHAIN: A, B; DNA (20-MER); CHAIN: C, D;	COMPLEX (DNA BINDING PROTEIN/DNA) DNA BINDING, COMPLEX (DNA BINDING PROTEIN/DNA)
1645	9ant	A	105	160	1.7e-25	0.55	0.66		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D,	COMPLEX (DNA-BINDING PROTEIN/DNA) HD;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									E, F;	HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1645	9ant	A	19	74	5.1e-29	0.46	0.78		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1646	1aut	L	261	326	0.00024	0.03	0.33		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1646	1dva	L	261	326	0.0006	-0.18	0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1646	1eis	A	115	200	7.2e-09	-0.02	0.11		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1646	1eis	A	196	270	6e-05	0.15	0.07		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1646	1ext	A	98	249	2.4e-14			63.01	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SUPERANTIGEN SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1646	1pfx	L	10	144	2.4e-13			64.18	FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1647	1quu	A	21	148	6e-08	0.08	-0.20		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1649	1aab		93	173	2.4e-16	0.61	0.39		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1649	1aab		94	151	1.7e-09	-0.00	0.54		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1649	1cg7	A	80	172	3.4e-12			51.42	NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1649	1cg7	A	85	152	3.4e-12	-0.05	0.81		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
1649	1ckt	A	100	173	6e-14	0.25	-0.08		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
1649	1hme		95	170	1.1e-12			51.33	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING 1HME 3 HMGB-BOX DOMAIN B OF RAT HMGB1) (NMR, 1 STRUCTURE) 1HME 4	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1649	1hme		95	177	3.4e-09	0.41	0.18		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING 1HME 3 HMGB-BOX DOMAIN B OF RAT HMGB1) (NMR, 1 STRUCTURE) 1HME 4	
1649	1hme		97	148	1.1e-12	0.12	0.87		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING 1HME 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									HMG-BOX DOMAIN B OF RAT HMG1) (NMR, 1 STRUCTURE) 1HME 4	
1649	1hsm		100	148	1.2e-11	0.22	0.89		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH 1HSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) 1HSM 4	
1649	1hsm		220	295	1.2e-12	-0.06	0.01		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH 1HSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) 1HSM 4	
1649	1hsm		98	179	1.7e-08	-0.10	0.24		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH 1HSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) 1HSM 4	
1649	1qrv	A	100	141	2.4e-10	0.31	0.21		DNA (5'-D(*GP*CP*GP*AP*TP*AP*TP*CP *GP*C)-3'); CHAIN: C, D; HIGH MOBILITY GROUP PROTEIN D; CHAIN: A, B;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMG-D
1649	1qrv	A	98	168	1.7e-07	0.29	0.63		DNA (5'-D(*GP*CP*GP*AP*TP*AP*TP*CP *GP*C)-3'); CHAIN: C, D; HIGH MOBILITY GROUP PROTEIN D;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	CHROMOSOMAL PROTEIN HMG-D
1649	2lef	A	101	179	2.4e-15	0.15	0.47		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1651	1alh	A	194	274	1.5e-30	0.30	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1651	1alh	A	194	276	1.6e-34			73.66	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1651	1alh	A	63	151	3.4e-21	-0.11	0.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1651	1alh	A	99	171	5.1e-25	0.01	-0.01		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1651	1mey	C	193	274	5.1e-51			83.90	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1651	1mey	C	193	274	5.1e-51	0.43	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1651	1mey	C	62	151	3.4e-40	0.17	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1651	1tf6	A	99	274	4e-34			67.48	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1651	1ubd	C	166	274	1.8e-34			71.38	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1651	2gli	A	126	277	1.6e-38			82.80	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1660	1cex		132	307	2.4e-11	0.59	-0.14		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1660	1cex		48	201	3.6e-08	0.21	-0.17		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1660	1cex		64	290	1.2e-10	0.70	-0.15		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1660	1d0s	A	23	172	4.8e-15	0.19	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1660	1d0s	A	34	363	7.2e-42	0.27	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1660	1eut		175	396	1.2e-08	0.20	-0.17		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										HYDROLASE, GLYCOSIDASE
1660	1eut		230	392	4.8e-09	0.19	-0.18		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1660	1qsa	A	873	967	7.2e-05	-0.10	0.11		SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA-SUPERHELIX, TRANSFERASE
1660	2tbv	C	139	412	8.4e-09	0.22	-0.19		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1660	2vsg	A	133	411	4.8e-12	0.09	-0.19		VARIANT SURFACE GLYCOPROTEIN ILTAT 1.24; CHAIN: A, B;	MEMBRANE PROTEIN VSG VSG, TRYPAPOSOME, ANTIGENIC VARIATION, MEMBRANE PROTEIN
1660	4ubp	C	32	445	4.8e-19	0.09	-0.19		UREASE (CHAIN A); CHAIN: A; UREASE (CHAIN B); CHAIN: B; UREASE (CHAIN C); CHAIN: C;	HYDROLASE UREA AMINOHYDROLASE; UREA AMINOHYDROLASE; UREA AMINOHYDROLASE; UREASE, BACILLUS PASTEURII, NICKEL, ACETOHYDROXAMIC ACID, 2 METALLOENZYME
1668	1d5r	A	6	137	8.5e-17	0.26	0.57		PHOSPHONOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
1668	1mkp		6	139	3.4e-16	0.10	0.49		PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP

Table 5

SFQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										KINASE HYDROLASE
1674	1zbd	B	311	367	0.004	0.07	0.37		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1674	1zbd	B	313	358	0.00085	0.29	0.15		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1704	1c2a	A	3	103	9.6e-15	0.89	-0.18		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1704	1c2a	A	3	103	9.6e-15	0.89	-0.18		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1704	1dx5	I	4	103	6e-11	0.99	-0.12		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN	SERINE PROTEINASE COAGULATION FACTOR II;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1704	1dx5	I	4	103	6e-11	0.99	-0.12		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1704	1eis	A	1	62	4.8e-13	1.29	0.04		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1704	1eis	A	1	62	4.8e-13	1.29	0.04		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1704	1eis	A	6	101	1.2e-17	0.91	-0.08		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1704	1eis	A	6	101	1.2e-17	0.91	-0.08		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUPERANTIGEN SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1704	1ext	A	2	103	1.2e-09	0.51	-0.13		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1704	1ext	A	2	103	1.2e-09	0.51	-0.13		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1704	1nub	A	3	102	3.6e-16	0.57	-0.19		BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	EXTRACELLULAR MODULE OSTEOONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES
1704	1nub	A	3	102	3.6e-16	0.57	-0.19		BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	EXTRACELLULAR MODULE OSTEOONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GLYCOSYLATED 3 PROTEIN MODRES
1704	1pfx	L	16	103	1.2e-11	0.36	-0.12		FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1704	1pfx	L	16	103	1.2e-11	0.36	-0.12		FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1704	1qub	A	2	103	8.4e-16	0.97	-0.19		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1704	1qub	A	2	103	8.4e-16	0.97	-0.19		HUMAN BETA2-GLYCOPROTEIN	MEMBRANE ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									I; CHAIN: A;	SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1704	1tpg		4	91	3.6e-07	1.31	0.04		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1704	1tpg		4	91	3.6e-07	1.31	0.04		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1706	1ciu		1025	1309	7.2e-22	0.18	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1706	1ciu		1150	1485	2.4e-25	0.00	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1706	1ciu		1204	1570	3.6e-26	0.15	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1706	1ciu		1348	1677	2.4e-25	0.20	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1706	1ciu		1380	1736	4.8e-25	0.02	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1706	1ciu		1429	1792	2.4e-26	0.02	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1706	1ciu		1492	1824	1.1e-22	0.03	-0.19		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		1572	1915	2.4e-24	0.06	-0.18		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		1633	1933	2.4e-21	0.03	-0.19		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		315	677	8.4e-27	0.13	-0.18		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		408	746	9.6e-28	0.12	-0.20		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		469	778	8.4e-27	0.16	-0.20		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		552	886	6e-28	0.19	-0.20		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		601	965	3.6e-26	0.09	-0.20		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1ciu		757	1060	7.2e-22	0.01	-0.20		6 CHAIN: NULL; 1CIU 7 CYCLODEXTRIN	1CIU 14 GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE
1706	1cyg		1091	1533	7.2e-32	0.01	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1706	1cyg		1241	1677	1.2e-30	0.07	-0.19		(E.C.2.4.1.19) (CGTASE) 1CYG 3	
									GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		1420	1840	6e-28	0.15	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		1485	1920	1.2e-27	0.01	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		186	548	3.6e-29	0.06	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		420	858	8.4e-31	0.17	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		495	884	2.4e-32	0.20	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		544	961	4.8e-31	0.10	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1cyg		752	1206	1.1e-26	0.14	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN	

Table 5

SEQ ID NO:	PDB ID	CCHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1706	1cyg		838	1293	2.4e-29	0.18	-0.20		GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1leap	B	1707	1791	0.0024	0.21	0.18		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1706	1edq	A	1203	1290	0.00012	-0.17	0.07		CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] 1EAP 3 PHOSPHONATE 1EAP 4	HYDROLASE BETA-ALPHA (TTM) BARREL
1706	1eut		1103	1345	2.4e-18	0.06	-0.19		CHITINASE A; CHAIN: A;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		1210	1455	2.4e-17	0.05	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		1313	1565	1.2e-19	0.03	-0.18		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		1389	1617	3.6e-22	0.30	-0.18		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		1437	1677	8.4e-20	0.12	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE,

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1706	1eut		1514	1835	1.2e-19	0.18	-0.17		SIALIDASE; CHAIN: NULL;	GLYCOSIDASE HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		1658	1933	9.6e-15	0.08	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		462	789	2.4e-22	0.08	-0.17		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		609	860	2.4e-20	0.08	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		686	1217	1.2e-16	0.10	-0.15		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		926	1289	6e-17	-0.00	-0.18		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1eut		989	1309	2.4e-16	0.02	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1706	1qun	B	1255	1521	2.4e-35	0.01	-0.17		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	1338	1613	9.6e-37	0.09	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	1402	1697	1.1e-35	0.16	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	1450	1745	3.6e-34	0.19	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	1514	1808	8.4e-32	0.29	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	350	645	1.2e-34	0.13	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									FIMH; CHAIN: B, D, F, H, J, L, N, P;	COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	414	693	6e-37	0.16	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	509	785	1.1e-37	0.22	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	558	837	9.6e-35	0.09	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	670	965	2.4e-34	0.15	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1706	1qun	B	925	1230	7.2e-35	0.01	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									P;	CHAPERONE/STRUCTURAL PROTEIN
1706	2tbv	C	1039	1357	9.6e-34	0.04	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	1253	1568	9.6e-40	0.04	-0.19		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	1384	1709	1.2e-41	0.20	-0.19		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	1577	1888	8.4e-37	0.09	-0.19		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	173	433	6e-23	0.11	-0.18		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	249	529	1.2e-34	0.10	-0.18		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	377	705	1.2e-41	0.11	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	733	1060	6e-38	0.00	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1706	2tbv	C	985	1326	8.4e-33	0.08	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1733	1bu2	A	49	273	4.4e-12			54.78	CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN
1733	1jkw		31	304	0.0022			65.17	CYCLIN H; CHAIN: NULL;	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1733	1qmr	B	110	292	1.1e-10	-0.50	0.00		CELL DIVISION PROTEIN	COMPLEX (PROTEIN)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	KINASE/CYCLIN CYCLIN-DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX
1733	1vin		110	222	8.8e-10	-0.65	0.06		CYCLIN A; CHAIN: NULL;	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2 BINDING PROTEIN
1733	1vin		28	313	8.8e-10			56.74	CYCLIN A; CHAIN: NULL;	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2 BINDING PROTEIN
1734	1aww		569	630	1.3e-12	0.87	0.74		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
1734	1cii		35	614	1.5e-05			76.29	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1734	1csk	A	574	626	2.2e-13	0.69	0.99		PHOSPHOTRANSFERASE C-SRC KINASE (SH3 DOMAIN)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1734	1cun	A	63	242	2.2e-06	0.05	0.10		(E.C.2.7.1.112) ICSK 3 ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN
1734	1fyn	A	574	626	4.4e-12	0.15	0.95		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO- ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP- BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PE PTIDE)
1734	1gbq	A	574	628	6.6e-14	0.73	0.99		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
1734	1gbr	A	566	628	1.3e-13	0.74	0.88		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1734	1hsq		569	636	2.2e-13	0.58	0.35		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
1734	1nlo	C	573	626	8.8e-14	0.67	0.99		C-SRC; CHAIN: C; NL1 (MN7- MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1734	1qly	A	571	626	6.6e-12	0.51	0.87		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1734	4hck		574	626	6.6e-12	0.14	0.96		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1750	1cj0	A	26	258	1.7e-30	-0.19	0.17		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE, 1 CARBON METABOLISM
1750	1cs1	A	3	185	1.2e-14	-0.28	0.23		CYSTATHIONINE GAMMA-	LYASE CGS; LYASE, LLP-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SYNTHASE; CHAIN: A, B, C, D;	DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS
1750	1dfo	A	2	255	3.4e-40	0.09	0.10		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
1764	1aif	H	802	896	0.0006	0.33	0.53		ANTI-IDIOTYPIC FAB 409.5.3 (1GG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN C REGION, V REGION
1764	1cgt		1004	1199	4e-10	0.38	-0.11		GLYCOSYLTRANSFERASE CYCLODEXTRIN (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		129	393	4e-12	0.20	-0.15		GLYCOSYLTRANSFERASE CYCLODEXTRIN (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		221	476	2e-12	0.01	-0.15		GLYCOSYLTRANSFERASE CYCLODEXTRIN (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		296	505	2e-12	0.00	-0.15		GLYCOSYLTRANSFERASE CYCLODEXTRIN (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		352	561	1e-12	0.25	-0.15		GLYCOSYLTRANSFERASE CYCLODEXTRIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1764	1cgt		381	617	4e-16	0.32	-0.15		(E.C.2.4.1.19) ICGT 3 GLYCOSYLTRANSFERASE CYCLODEXTRIN	
1764	1cgt		430	700	1.6e-12	0.10	-0.18		GLYCOSYLTRANSFERASE (E.C.2.4.1.19) ICGT 3 CYCLODEXTRIN	
1764	1cgt		44	283	2e-10	0.10	-0.18		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLYCOSYLTRANSFERASE (E.C.2.4.1.19) ICGT 3	
1764	1cgt		512	754	6e-11	0.18	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLYCOSYLTRANSFERASE (E.C.2.4.1.19) ICGT 3	
1764	1cgt		584	841	4e-12	0.06	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLYCOSYLTRANSFERASE (E.C.2.4.1.19) ICGT 3	
1764	1cgt		684	894	6e-11	0.19	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLYCOSYLTRANSFERASE (E.C.2.4.1.19) ICGT 3	
1764	1cgt		739	943	4e-14	0.30	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLYCOSYLTRANSFERASE (E.C.2.4.1.19) ICGT 3	
1764	1cgt		746	1007	1.4e-09	0.24	-0.17		GLYCOSYLTRANSFERASE CYCLODEXTRIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									GLYCOSYLTRANSFERASE (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		8	203	6e-11	0.45	-0.12		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLYCOSYLTRANSFERASE (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		801	1035	1e-09	0.14	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLYCOSYLTRANSFERASE (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		830	1090	1.8e-11	0.21	-0.18		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLYCOSYLTRANSFERASE (E.C.2.4.1.19) 1CGT 3	
1764	1cgt		885	1155	1.2e-12	0.25	-0.12		GLYCOSYLTRANSFERASE CYCLODEXTRIN	
									GLYCOSYLTRANSFERASE (E.C.2.4.1.19) 1CGT 3	
1764	1ciu		124	434	1.4e-24	0.20	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		165	532	1.4e-22	0.21	-0.12		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		2	339	1e-24	0.22	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		221	564	8e-25	0.27	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		301	643	6e-26	0.14	-0.20		CYCLODEXTRIN	GLYCOSIDASE CGTASE;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	FMF score	SEQ FOLD score	Compound	PDB annotation
									GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		326	700	1.8e-24	0.21	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		431	841	4e-26	0.16	-0.14		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		503	863	4e-24	0.24	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		625	1007	2e-27	0.39	-0.12		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		73	475	8e-23	0.22	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		732	1040	6e-25	0.23	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		768	1126	2e-25	0.12	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1ciu		947	1197	4e-10	0.15	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
1764	1cwv	A	18	532	4e-53	0.33	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
1764	1cwv	A	193	699	1.4e-51	0.25	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1764	1cwv	A	281	783	4e-52	0.23	-0.18		INVASIN; CHAIN: A;	PROTEIN, INV GENE
1764	1cwv	A	364	883	4e-54	0.40	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING
1764	1cwv	A	445	948	4e-54			105.80	INVASIN; CHAIN: A;	PROTEIN, INV GENE
1764	1cwv	A	493	1006	8e-54	0.27	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING
1764	1cwv	A	613	1091	1e-52	0.28	-0.18		INVASIN; CHAIN: A;	PROTEIN, INV GENE
1764	1cwv	A	670	1175	1e-50	0.39	-0.17		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING
1764	1cwv	A	866	1196	4e-35	0.28	-0.19		INVASIN; CHAIN: A;	PROTEIN, INV GENE
1764	1cwv	A	98	638	4e-52	0.24	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING
1764	1cyg		125	587	1.2e-27	0.21	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	PROTEIN, INV GENE
1764	1cyg		2	204	2e-16	0.13	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN	STRUCTURAL PROTEIN INTEGRIN-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1764	1cyg		23	476	6e-28	0.01	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1764	1cyg		243	691	4e-30	0.33	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1764	1cyg		456	868	1.2e-29	0.33	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1764	1cyg		548	1015	1e-37	0.15	-0.20		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1764	1cyg		761	1197	2e-20	0.21	-0.18		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
1764	1d3c	A	218	476	6e-10	0.23	0.05		CYCLODEXTRIN GLYCOSYLTRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-AMYLASE, PRODUCT COMPLEX, OLIGOSACCHARIDE, FAMILY 13 2 GLYCOSYL HYDROLASE, TRANSGLYCOSYLATION, INDUCED FIT, 3 CATALYSIS, TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	F _{MF} score	SEQ FOLD score	Compound	PDB annotation
1764	1d3c	A	379	617	2e-10	0.52	-0.14		CYCLODEXTRIN GLYCOSYLTRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-AMYLASE, PRODUCT COMPLEX, OLIGOSACCHARIDE, FAMILY 13 2 GLYCOSYL HYDROLASE, TRANSGLYCOSYLATION, INDUCED FIT, 3 CATALYSIS, TRANSFERASE
1764	1d3c	A	567	841	4e-08	0.20	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-AMYLASE, PRODUCT COMPLEX, OLIGOSACCHARIDE, FAMILY 13 2 GLYCOSYL HYDROLASE, TRANSGLYCOSYLATION, INDUCED FIT, 3 CATALYSIS, TRANSFERASE
1764	1d3c	A	817	1089	4e-09	0.22	-0.20		CYCLODEXTRIN GLYCOSYLTRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-AMYLASE, PRODUCT COMPLEX, OLIGOSACCHARIDE, FAMILY 13 2 GLYCOSYL HYDROLASE, TRANSGLYCOSYLATION, INDUCED FIT, 3 CATALYSIS, TRANSFERASE
1764	1d3c	A	869	1124	1.2e-08	0.21	-0.18		CYCLODEXTRIN GLYCOSYLTRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-AMYLASE, PRODUCT COMPLEX, OLIGOSACCHARIDE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	FMF score	SEQ FOLD score	Compound	PDB annotation
										FAMILY 13 2 GLYCOSYL HYDROLASE, TRANSGLYCOSYLATION, INDUCED FIT, 3 CATALYSIS, TRANSFERASE
1764	1d3c	A	88	340	4e-09	0.08	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-AMYLASE, PRODUCT COMPLEX, OLIGOSACCHARIDE, FAMILY 13 2 GLYCOSYL HYDROLASE, TRANSGLYCOSYLATION, INDUCED FIT, 3 CATALYSIS, TRANSFERASE
1764	1eut		17	232	1.6e-16	0.05	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		190	464	1.6e-18	0.32	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		190	617	2e-16	0.33	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		33	411	1.2e-16	0.36	-0.18		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		365	765	1.6e-18	0.31	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		501	854	2e-20	0.39	-0.15		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		60	371	4e-20	0.33	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		600	1198	1.2e-18			151.40	SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		656	922	2e-18	0.21	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		693	1145	1.2e-18	0.22	-0.17		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1eut		766	1185	4e-17	0.36	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1764	1pam	A	153	574	6e-33	0.40	-0.20		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1764	1pam	A	236	620	8e-30	0.22	-0.19		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
1764	1pam	A	406	841	6e-33	0.23	-0.20		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
1764	1pam	A	483	884	8e-33	0.39	-0.19		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
1764	1pam	A	595	1007	6e-33	0.26	-0.20		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
1764	1pam	A	734	1159	8e-32	0.17	-0.20		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
1764	1pam	A	8	382	8e-30	0.30	-0.17		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
1764	1qq4	A	778	962	1.6e-05	0.20	0.04		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1764	1qun	B	1000	1196	1.8e-18	0.25	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									P;	CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	130	412	8e-33	0.18	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	16	320	8e-31	0.26	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	242	561	2e-31	0.18	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	327	617	1.8e-33	0.25	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	4	179	1.4e-14	0.08	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1764	1qun	B	418	699	2e-32	0.34	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	PROTEIN CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	464	764	1e-35	0.24	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	600	886	2e-30	0.17	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	654	943	4e-30	0.21	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	721	1012	1e-31	0.26	-0.18		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1764	1qun	B	74	358	8e-32	0.27	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	765	1051	4e-34	0.22	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	821	1127	8e-33	0.34	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	901	1164	1e-33	0.25	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	1qun	B	966	1183	4e-21	0.16	-0.20		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1764	2tbv	C	18	340	8e-34	0.11	-0.20		VIRUS TOMATO BUSHY STUNT	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1764	2tbv	C	307	643	1.8e-34	0.19	-0.20		VIRUS 2TBV 4	
1764	2tbv	C	447	775	1.4e-36	0.29	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1764	2tbv	C	661	995	4e-38	0.19	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1764	2tbv	C	836	1166	6e-34	0.25	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1764	2tbv	C	89	441	4e-35	0.19	-0.20		VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
1769	1ddv	A	13	121	6.8e-27	0.33	0.39		GLGF-DOMAIN PROTEIN HOMER; CHAIN: A; METABOTROPIC GLUTAMATE RECEPTOR MGLURS; CHAIN: B; GLGF-DOMAIN PROTEIN HOMER; CHAIN: A;	SIGNALING PROTEIN PROTEIN-LIGAND COMPLEX, POLYPROLINE RECOGNITION, BETA TURN SIGNALING PROTEIN PLECKSTRIN HOMOLOGY DOMAIN FOLD
1769	1ddw	A	8	122	6.8e-30	0.79	0.84		VASODILATOR-STIMULATED PHOSPHOPROTEIN; CHAIN: A;	SIGNALING PROTEIN VASP; EVH1, VASP-ENA, NMR, POLY-PROLINE-BINDING DOMAIN
1769	1egx	A	8	124	1.2e-36	0.94	1.00		MENA EVH1 DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	CONTRACTILE PROTEIN WH1 DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN
1769	1evh	A	9	122	6.8e-38	0.93	1.00	83.11	MENA EVH1 DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	CONTRACTILE PROTEIN WH1 DOMAIN; MOLECULAR RECOGNITION, ACTIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1769	1qc6	A	8	119	1.7e-32	0.93	1.00		EVH1 DOMAIN FROM ENA/VASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE-PRO-PRO-PRO-THR-ASP-GLU-GLU; CHAIN: C, D;	DYNAMICS, CONTRACTILE PROTEIN
1769	1qc6	A	9	121	1.7e-32			62.45	EVH1 DOMAIN FROM ENA/VASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE-PRO-PRO-PRO-THR-ASP-GLU-GLU; CHAIN: C, D;	CELL MOTILITY AN INCOMPLETE SEVEN STRANDED ANTI-PARALLEL BETA BARREL 2 CLOSED BY AN ALPHA HELIX, EVH1 DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE
1772	1gof		183	449	8e-23	-0.16	0.23		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1772	1gof		344	450	0.0041	0.03	0.16		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1775	1a4y	A	9	154	4e-16	-0.25	0.23		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										(INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1775	1a9n	A	126	195	1e-08	-0.28	0.16		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	A	3	107	1e-09	0.20	0.69		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	A	32	169	4e-22	0.67	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	A	5	122	2e-20	0.42	0.76		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	C	126	195	1.2e-08	-0.10	0.47		U2 RNA HAIRPIN IV; CHAIN: Q,	COMPLEX (NUCLEAR

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	C	3	107	1e-09	0.37	0.87		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	C	32	169	8e-23	0.37	0.93		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1a9n	C	5	122	2e-20	0.50	0.88		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1775	1d0b	A	1	128	1e-26	0.65	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1775	1d0b	A	21	192	5.1e-28	0.22	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1775	1d0b	A	47	238	1.4e-20	0.05	0.75		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1775	1d0b	A	8	197	4e-31	0.18	0.70		INTERNALIN B; CHAIN: A;	BINDING, CELL ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1775	1dce	A	144	197	1.7e-11	-0.13	0.93		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1775	1dce	A	23	128	1.7e-13	0.32	0.98		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1775	1dce	A	5	106	1.2e-15	0.62	0.93		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1775	1dce	A	74	197	3.4e-11	-0.30	0.11		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN:	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSF

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	ERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1775	1ds9	A	1	106	5.1e-16	-0.37	0.11		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1775	1ds9	A	83	197	5.1e-17	-0.65	0.18		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1775	1fo1	A	46	123	1.7e-07	0.25	0.58		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1775	1fo1	B	145	197	3.4e-06	-0.78	0.37		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1775	1fqv	A	51	193	1e-09	0.09	0.25		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									N, P;	CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1775	1fs2	A	5	189	2e-22	-0.05	0.75		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1775	1fs2	A	51	193	1e-09	-0.11	0.33		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1775	1yrg	A	5	196	2e-20	0.02	0.37		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1775	2bnh		8	195	1e-24	-0.01	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGEN IN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1777	1az5		248	348	3.4e-23	0.30	0.77		SIV PROTEASE; CHAIN: NULL;	ASPARTYL PROTEASE SIV PROTEINASE; HIV, AIDS, PROTEINASE, ASPARTYL PROTEASE, ENDONUCLEASE
1777	1bai	A	233	347	4.8e-18			60.31	ROUS SARCOMA VIRUS PROTEASE; CHAIN: A, B; INHIBITOR; CHAIN: C;	COMPLEX (PROTEASE/INHIBITOR) HUMAN IMMUNODEFICIENCY VIRUS PROTEASE, ROUS SARCOMA VIRUS 2 PROTEASE, CRYSTAL STRUCTURES, PROTEIN-MEDIATED INTERACTION, 3 VIRAL MATURATION, COMPLEX (PROTEASE/INHIBITOR) HEADER
1777	1bdq	A	244	348	3.4e-39	0.28	0.48		HIV-1 PROTEASE; CHAIN: A, B;	HYDROLASE HYDROLASE, AIDS, POLYPROTEIN, ASPARTYL PROTEASE, ACID 2 PROTEASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										HYDROXYETHYLENE ISOSTERE INHIBITOR, SUBSTRATE 3 ANALOGUE INHIBITOR
1777	1bwb	A	244	348	3.4e-40	0.30	0.57		HIV-1 PROTEASE; CHAIN: A, B;	HYDROLASE HIV-1 PROTEASE, HYDROLASE
1777	1daz	C	244	348	1.7e-38	0.11	0.65		PEPTIDE INHIBITOR; CHAIN: A, B; HIV-1 PROTEASE (RETROPEPSIN); CHAIN: C, D;	HYDROLASE HIV-1 PROTEASE, MUTANT, DIMER, INHIBITOR, OCCUPANCY
1777	1dun		119	228	3.4e-23	0.32	1.00		DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEODITOHYDROLASE; CHAIN: NULL;	HYDROLASE DUTPASE, DUTP PYROPHOSPHATASE; HYDROLASE, DUTPASE, EIAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1777	1dun		120	218	1.2e-26	0.54	1.00		DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEODITOHYDROLASE; CHAIN: NULL;	HYDROLASE DUTPASE, DUTP PYROPHOSPHATASE; HYDROLASE, DUTPASE, EIAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1777	1euw	A	124	228	1.7e-16	0.51	0.68		DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE; CHAIN: A;	HYDROLASE DUTPASE; JELLY ROLL, MERCURY DERIVATIVE
1777	1f7d	A	119	226	6.8e-23	0.35	1.00		POL POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1777	1f7r	A	119	242	8.5e-24	-0.01	1.00		POL POLYPROTEIN; CHAIN: A;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA BARREL PROTEIN
1777	1f7r	A	122	234	6e-28	0.13	1.00		POL POLYPROTEIN; CHAIN: A;	VIRUS/VIRAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										EIGHT STRANDED BETA BARREL PROTEIN
1777	1fmb		244	348	1.2e-14			58.04	EIAV PROTEASE; CHAIN: NULL;	HYDROLASE (ACID PROTEINASE) HYDROLASE (ACID PROTEINASE), RNA-DIRECTED DNA POLYMERASE, 2 ASPARTYL PROTEASE, ENDONUCLEASE, POLYPROTEIN
1777	1g6l	A	179	348	1.7e-42	0.36	0.35		HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1777	1hvc		122	348	6.8e-43			57.17	HYDROLASE (ACID PROTEASE) HIV-1 PROTEASE (TETHERED DIMER LINKED BY 1HVC 3 GLY-SER-SER-SER-SER GLY) COMPLEXED WITH A-76928 1HVC 4	
1777	1hvc		177	348	6.8e-43	0.16	0.37		HYDROLASE (ACID PROTEASE) HIV-1 PROTEASE (TETHERED DIMER LINKED BY 1HVC 3 GLY-SER-SER-SER-SER GLY) COMPLEXED WITH A-76928 1HVC 4	
1777	1ida	A	244	347	6.8e-26	0.22	0.64		HYDROLASE (ACID PROTEINASE) HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (HIV-2) PROTEASE 1IDA 3 COMPLEXED WITH THE INHIBITOR BILA 1906 CONTAINING THE 1IDA 4 HYDROXYETHYLAMINE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1777	1mtr	A	244	342	6.8e-38	0.25	0.92		DIPEPTIDE ISOSTERE IIDA 5 HIV-1 PROTEASE; A CYCLIC PHE-ILE-VAL PEPTIDOMIMETIC INHIBITOR; CHAIN: C;	COMPLEX (ASPARTYL PROTEASE/INHIBITOR) HIV-1 PR; HYDROLASE, ASPARTYL PROTEINASE, AIDS, PEPTIDE, INHIBITOR
1777	1sip		244	348	3.4e-27	-0.05	0.30		HYDROLASE(ACID PROTEINASE) SIMIAN IMMUNODEFICIENCY VIRUS (SIV) PROTEINASE 1SIP 3 (SIV MAC251-32H ISOLATE) (E.C.3.4.23.-) 1SIP 4	
1788	1akh	B	70	138	1.4e-14	-0.37	0.13		MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA-BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
1788	1akh	B	72	137	1.1e-15	-0.58	0.16		MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA-BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
1788	1apl	C	70	129	2.4e-15	-0.49	0.28		COMPLEX(DNA BINDING PROTEIN/DNA) MAT ALPHA2	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1788	1apl	C	73	129	8.5e-14	-0.05	0.18		HOMEODOMAIN COMPLEXED WITH OPERATOR DNA 1APL 3	
1788	1b72	B	72	134	1.4e-20	-0.20	0.46		COMPLEX(DNA BINDING PROTEIN/DNA) MAT ALPHA2 HOMEODOMAIN COMPLEXED WITH OPERATOR DNA 1APL 3	
1788	1b8i	B	74	131	6.8e-19	0.12	0.92		HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1788	1du6	A	75	131	1.5e-17	0.19	0.88		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1788	1mm	C	54	129	6.8e-15	-0.16	0.10		HOMEBOX PROTEIN PBX1; CHAIN: A; MCM1 TRANSCRIPTIONAL REGULATOR; CHAIN: A, B; MAT ALPHA-2 TRANSCRIPTIONAL REPRESSOR; CHAIN: C, D; STE6 OPERATOR DNA; CHAIN: E, F;	GENE REGULATION PBX1; HOMEODOMAIN COMPLEX (TRANSCRIPTION/HOMEBOX/DNA) PHEROMONE RECEPTOR TRANSCRIPTION FACTOR; MATING-TYPE PROTEIN ALPHA-2; TRANSCRIPTION REGULATION, TRANSCRIPTIONAL REPRESSION, 2 DNA-BINDING PROTEIN, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									(TRANSCRIPTION/HOMEBOX/DNA)	
1792	1b7f	A	154	323	8e-44			96.30	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1792	1b7f	A	157	323	8e-44	0.89	1.00		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1792	1b7f	A	248	425	4e-43	0.81	1.00		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1792	1b7f	A	3	131	1.7e-30	-0.20	0.29		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1792	1cvj	A	157	329	1.6e-45	0.87	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	A	158	329	1.4e-27	1.04	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1792	1cvj	A	249	426	4e-43	1.01	1.00		F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	A	250	422	1.2e-28	0.97	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	A	68	236	8.5e-55			223.38	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	A	69	236	8.5e-55	0.81	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	B	157	313	1.6e-37	1.06	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	B	158	309	6.8e-23	0.83	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	B	249	417	6e-38	0.93	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	B	3	130	6.8e-29	-0.03	0.06		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	B	68	222	3.4e-46			188.53	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	B	69	216	3.4e-46	0.89	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	REGULATION/RNA
1792	1cvj	F	157	301	8e-30	0.86	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	F	249	403	4e-28	0.56	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	H	157	302	6e-31	0.69	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cvj	H	249	403	2e-28	0.86	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1792	1cx0	A	352	427	6e-21	0.87	1.00		U1A PROTEIN; CHAIN: A; HDV RIBOZYME SELF-CLEAVED; CHAIN: B;	RNA BINDING PROTEIN/RNA NESTED DOUBLE PSEUDOKNOT RNA STRUCTURE
1792	1d8z	A	352	427	2e-21	0.85	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1792	1d8z	A	64	146	8.5e-23	0.20	0.87		HU ANTIGEN C; CHAIN: A;	RNA-BINDING DOMAIN
1792	1d9a	A	352	427	1e-20	1.04	1.00		HU ANTIGEN C; CHAIN: A;	RNA-BINDING DOMAIN
1792	1ftt		352	427	4e-20	0.74	1.00		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME
1792	1ftt		63	160	1.4e-11	0.55	0.47		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME
1792	1fj7	A	352	427	2e-20	0.53	0.31		NUCLEOLIN RBD1; CHAIN: A;	STRUCTURAL PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1792	1fj7	A	52	146	4e-16	0.23	-0.02		NUCLEOLIN RBD1; CHAIN: A;	STRUCTURAL PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1792	1ha1		151	324	4e-41			87.90	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2
1792	1ha1		157	323	4e-41	0.91	1.00		HNRNP A1; CHAIN: NULL;	RIBONUCLEOPROTEIN NUCLEAR PROTEIN HETEROGENEOUS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1792	1ha1		246	425	1.6e-38	0.46	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1792	1ha1		248	425	1.2e-31	0.85	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1792	1ha1		5	143	1.5e-35	0.07	0.09		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1792	1nrc	A	352	427	1.8e-20	-0.09	1.00		RIBONUCLEOPROTEIN PROTEIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									FROM U1 SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	
1792	1qm9	A	157	327	4e-40	0.44	0.99		POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
1792	1qm9	A	248	426	1.6e-39	0.19	0.74		POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
1792	1sxl		339	428	2e-20			55.90	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD- 2), RESIDUES 199 - 294 PLUS N- TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1792	1sxl		349	427	2e-20	0.78	1.00		RNA-BINDING PROTEIN SEX-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1792	1sxl		56	131	1.2e-16	-0.03	0.49		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1792	1urn	A	352	427	1.2e-20	1.14	1.00		U1A SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 2IMER HAIRPIN (5'-(AP*AP*UP*CP*CP*AP*UP*UP*1URN 11 CHAIN: P, Q, R 1URN 13 SEX-LETHAL PROTEIN; CHAIN: NULL;	COMPLEX (RIBONUCLEOPROTEIN/RNA)
1792	2sxl		352	426	8e-22	0.86	1.00			RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1792	2u2f	A	352	426	2e-20	1.32	1.00		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1792	2up1	A	151	332	8e-44			99.86	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1792	2up1	A	156	333	1.7e-36	1.00	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	RIBONUCLEOPROTEIN A1 COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1792	2up1	A	157	330	8e-44	1.00	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1792	2up1	A	243	426	6e-44	0.81	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1792	2up1	A	248	425	5.1e-33	0.70	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										NUCLEAR 2 RIBONUCLEOPROTEIN A1
1792	2up1	A	5	150	1.2e-37	-0.05	0.18		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1792	3sxl	A	155	313	1.7e-23	0.84	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1792	3sxl	A	156	318	8e-43			93.55	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1792	3sxl	A	157	316	8e-43	0.77	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1792	3sxl	A	248	418	6e-40	0.63	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1807	1a7i		3	62	6.8e-16	-0.04	0.45		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1807	1a7i		4	60	4.8e-19			50.26	QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1807	1a7i		5	59	4.8e-19	0.02	0.53		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1807	1ark		166	225	1e-18			80.79	NEBULIN; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SH3 DOMAIN, NEBULIN, Z-DISK ASSEMBLY, 2 ACTIN- BINDING
1807	1ark		166	225	1e-18	0.56	1.00		NEBULIN; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SH3 DOMAIN, NEBULIN, Z-DISK ASSEMBLY, 2 ACTIN- BINDING
1807	1ark		168	225	1.2e-13	0.42	1.00		NEBULIN; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SH3 DOMAIN, NEBULIN, Z-DISK ASSEMBLY, 2 ACTIN- BINDING
1807	1awj		151	221	8.5e-12	0.20	0.41		ITK; CHAIN: NULL;	TRANSFERASE IL-2- INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1807	1awj		153	223	7.2e-17	0.31	0.45		ITK; CHAIN: NULL;	TRANSFERASE IL-2- INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1807	1b8t	A	5	74	8.5e-22	-0.08	0.72		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1807	1ctl		5	74	8.5e-22	-0.14	0.69		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1807	1cxx	A	2	60	1.2e-19			52.57	CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1807	1cxx	A	2	60	1.7e-18	0.38	0.80		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1807	1cxx	A	3	59	1.2e-19	0.27	0.76		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1807	1efn	A	171	225	5.1e-20	0.68	1.00		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF
1807	1fmk		168	224	5.1e-19	0.27	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1807	1fyn	A	166	225	1e-20	0.54	0.99		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1807	1gfc		167	225	6.8e-19	0.60	1.00		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1807	1gri	A	165	225	3.4e-19	0.69	0.99		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B;	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1807	1gri	A	18	225	4.8e-15			51.32	1GRI 6 GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1807	1gri	A	49	225	4.8e-15	0.16	-0.18		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1807	1iml		3	73	1.2e-21			55.79	CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1807	1iml		3	75	1.2e-21	0.32	0.62		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1807	1shf	A	171	225	1.7e-20	-0.17	0.98		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1807	1zfo		1	30	6.8e-09	-0.54	1.00		LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN
1807	1zfo		1	30	8.4e-12			56.91	LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN
1807	1zfo		1	30	8.4e-12	-0.54	1.00		LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN
1808	1aq1		70	367	0	0.58	1.00		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1808	1aq1		70	368	0			235.79	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1808	1bi8	A	71	358	3.4e-90			187.06	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1808	1bi8	A	72	358	3.4e-90	0.43	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1808	1blx	A	67	360	5.1e-98	0.69	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	HEADER HELIX COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1808	1blx	A	68	366	5.1e-98			213.62	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1808	1cmk	E	21	388	6.8e-54			109.44	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1808	1cmk	E	31	391	6.8e-54	0.09	0.68		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1808	1hcl		70	367	0	0.70	1.00		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1808	1hcl		70	368	0			269.62	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PHOSPHORYLATION PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1808	1qcf	A	51	316	1.4e-34	0.09	0.96		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1808	3erk		56	399	6e-99			197.73	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1808	3erk		67	361	6e-99	0.53	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1856	1alh	A	462	540	8.5e-25	-0.50	0.33		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	(ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1alh	A	495	572	2e-14	-0.53	0.04		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1alh	A	516	598	5.1e-29	-0.16	0.64		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1alh	A	546	626	1.2e-30	0.13	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1alh	A	574	654	1.5e-30	-0.16	0.95		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1alh	A	602	682	5.1e-30	-0.00	0.86		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1alh	A	602	684	3.4e-31			75.25	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SITE; CHAIN: B, C;	FINGER, DNA-BINDING PROTEIN
1856	1alh	A	658	736	3.4e-20	0.21	0.10		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1856	1bbo		688	737	5.1e-05	-0.11	0.15		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
1856	1buo	A	15	141	1.7e-37	0.25	0.95		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1856	1mey	C	461	540	6.8e-43	-0.36	0.22		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1856	1mey	C	515	598	6.8e-48	-0.14	0.53		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1mey	C	545	626	1.7e-49	0.23	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1mey	C	573	654	1.5e-49	0.19	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1mey	C	601	682	5.1e-50	0.15	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1mey	C	629	710	3.4e-50			83.92	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1mey	C	629	710	3.4e-50	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1mey	C	657	736	3.4e-37	0.32	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1856	1qsa	A	296	387	1.8e-08	0.27	-0.20		SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA-SUPERHELIX, TRANSFERASE
1856	1quu	A	301	380	4.4e-09	1.02	-0.20		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1856	1req	A	218	379	4.4e-14	0.15	-0.20		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
1856	1req	A	306	423	6.6e-18	0.73	-0.20		METHYLMALONYL-COA	ISOMERASE ISOMERASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1856	1sp2		686	714	6.8e-06	-0.25	0.37		MUTASE; CHAIN: A, B, C, D; SPIF2; CHAIN: NULL;	MUTASE, INTRAMOLECULAR TRANSFERASE ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1856	1tf3	A	462	540	8.5e-17	0.01	0.05		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1856	1tf3	A	546	626	3.4e-21	-0.22	0.59		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1856	1tf6	A	462	614	5.1e-34	-0.41	0.31		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1tf6	A	516	663	6.8e-37	-0.23	0.15		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1tf6	A	545	711	2.2e-44			98.94	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1tf6	A	546	691	1.7e-38	-0.12	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1tf6	A	546	707	2.2e-44	-0.07	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1ff6	A	575	716	1.5e-38	0.22	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1ff6	A	602	737	3.4e-30	0.20	0.54		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1856	1ubd	C	442	540	6.8e-27	-0.73	0.04		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1856	1ubd	C	469	570	3.4e-30	-0.62	0.01		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	493	626	8.8e-24	-0.36	0.25		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	496	598	1e-33	-0.35	0.55		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	547	655	5.1e-35			78.17	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	550	682	4.4e-31	-0.30	0.40		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	553	654	5.1e-35	0.11	0.96		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	609	710	5.1e-35	-0.12	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1856	1ubd	C	637	731	1.7e-25	0.12	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	1ubd	C	665	736	1.2e-13	-0.13	0.29		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1856	2adr		658	716	1.1e-19	-0.04	0.94		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1856	2gli	A	441	569	1.7e-26	-0.40	0.37		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	2gli	A	496	625	3.4e-33	-0.18	0.41		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	2gli	A	545	684	8.8e-42	-0.07	0.84		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	2gli	A	573	712	4.4e-42			85.38	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	2gli	A	575	707	4.4e-42	0.33	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	2gli	A	581	709	1.2e-34	0.12	0.68		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	2gli	A	609	736	1.7e-27	0.14	0.63		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1856	7znf		686	714	0.00012	-0.19	0.53		ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-SWAP) (NMR, 12 STRUCTURES)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									7ZNF 3	
1871	1a4y	A	100	479	1.5e-27	0.04	0.17		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1871	1a4y	A	160	591	3.4e-47			155.44	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1871	1a4y	A	201	590	3.4e-47	0.31	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1871	1a9n	A	289	366	6.8e-05	-0.44	0.09		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B';	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1871	1a9n	A	360	458	1e-06	0.37	0.16		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1871	1a9n	A	454	570	6e-05	-0.09	0.18		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1871	1a9n	C	454	570	0.00012	-0.10	0.54		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1871	1d0b	A	383	585	6.8e-17	-0.42	0.11		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1871	1d0b	A	550	589	0.0048	-0.41	0.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1871	1ds9	A	307	449	1e-09	-0.06	0.00		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1871	1fo1	A	507	571	0.0012	-0.74	0.03		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1871	1fo1	B	385	478	1.7e-06	0.15	0.01		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1871	1fo1	B	441	487	0.0036	-0.88	0.17		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1871	1fqv	A	363	578	1.4e-09	0.26	-0.13		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1871	1yrg	A	257	487	8.5e-13	0.22	0.30		GTPASE-ACTIVATING PROTEIN	TRANSCRIPTION RNAIP;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RNA1_SCHPO; CHAIN: A, B;	RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIREDAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1871	1yrg	A	296	571	3.4e-15	0.08	0.07		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIREDAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1871	1yrg	A	361	590	5.1e-17	0.48	1.00		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIREDAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1871	2bnh		143	591	1.7e-49			145.84	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										RIBONUCLEASE/ANGIOGEN IN INHIBITOR ACETYLATION, LEUCINE- RICH REPEATS
1871	2bnh		166	590	1.7e-49	0.12	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGEN IN INHIBITOR ACETYLATION, LEUCINE- RICH REPEATS
1886	1mai		12	127	3.4e-35	0.87	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
1886	1mai		12	127	3.4e-35	0.87	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
1886	1mai		9	128	3.4e-35			65.10	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
1886	1mai		9	128	3.4e-35			65.10	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, HYDROLASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
1898	1a1h	A	406	488	1.8e-44			88.83	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1898	1mey	C	349	431	1.7e-50			108.16	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1898	1tf6	A	293	461	1.4e-76			114.66	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1898	1ubd	C	319	431	2e-59			96.44	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1898	2gli	A	323	460	6e-74			107.35	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	1alh	A	107	185	5.1e-20	0.12	-0.18		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1937	1mey	C	106	186	3.4e-33	-0.29	0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	135	212	6.8e-36	-0.26	0.24		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	163	240	1.7e-36	0.09	0.86		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	187	268	6.8e-42	0.38	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	187	296	6e-42	-0.33	0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	215	296	5.1e-44	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	215	324	8e-42	0.08	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1mey	C	243	324	5.1e-45	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	271	352	1.5e-45	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	272	352	8e-46	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	299	380	5.1e-46	0.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	327	408	1e-46	0.15	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	355	436	5.1e-47	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	383	464	8.5e-47	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	411	492	3.4e-47	0.60	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	439	520	1.7e-48	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1mey	C	467	548	3.4e-49	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	495	576	1e-49	0.62	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	523	604	3.4e-50	0.34	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	551	632	1.4e-50	0.61	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	551	633	1e-50			103.75	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	579	660	1e-50	0.66	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	635	716	1e-50	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	663	744	1.7e-50	0.28	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	691	772	1.7e-50	0.36	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	C	719	785	1.7e-40	0.05	0.93		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1mey	G	185	212	5.1e-09	-0.14	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1937	1tf6	A	188	338	3.4e-34	0.08	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	188	352	6e-69	-0.07	0.82		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1tf6	A	272	417	3.4e-34	-0.12	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	272	436	1.2e-72	-0.05	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	328	473	3.4e-35	-0.18	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	356	501	3.4e-36	0.12	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1tf6	A	412	576	4e-71	-0.12	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	468	613	6.8e-37	0.42	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	468	632	2e-73	0.06	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	552	716	2e-73	0.01	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	579	742	2e-73			108.49	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	580	725	6.8e-38	0.25	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	608	772	2e-71	0.11	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1tf6	A	636	785	3.4e-37	0.27	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1937	1ubd	C	112	212	5.1e-24	-0.45	0.11		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	166	268	3.4e-28	0.12	0.75		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	195	296	6.8e-31	-0.19	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1ubd	C	248	353	4e-52	0.07	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	269	381	4e-55	0.02	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	297	408	4e-51	-0.00	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	382	492	1.8e-49	0.27	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	409	520	2e-52	0.08	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	447	548	5.1e-34	0.29	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	465	577	2e-56	0.10	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1ubd	C	497	604	6.8e-35	0.24	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	521	632	1e-56	0.31	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	578	689	1.2e-54	0.22	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	579	689	1.2e-54			94.34	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	605	745	1.2e-52	0.06	0.88		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	615	716	1.7e-34	0.35	0.99		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	640	744	3.4e-35	-0.05	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	1ubd	C	661	772	8e-52	0.08	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	1ubd	C	671	772	1.7e-34	0.01	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	2gli	A	114	242	1.7e-23	-0.25	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1937	2gli	A	135	267	5.1e-27	-0.18	0.58		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1937	2gli	A	166	326	2e-54	-0.17	0.66		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	187	354	8e-69	-0.03	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	272	409	1.2e-66	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	356	522	1e-67	0.05	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	383	550	1.2e-66	0.13	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	411	578	1e-69	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	467	606	6e-71	0.50	1.00		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	523	662	6e-71			96.67	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	551	690	6e-70	0.44	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	607	774	6e-70	0.13	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1937	2gli	A	643	771	6.8e-34	0.26	0.86		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1938	1ckl	A	264	321	1.2e-10	0.76	0.84		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1938	1ckl	A	61	117	2.4e-10	0.59	0.95		CD46; CHAIN: A, B, C, D, E, F;	MEASLES VIRUS, GLYCOPROTEIN
1938	1dx5	I	55	173	1.7e-12	0.25	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1938	1e5g	A	264	371	5.1e-11	0.64	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1938	1e5g	A	3	113	1.5e-09	0.03	-0.19		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1938	1e5g	A	61	186	1.2e-11	0.21	-0.18		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
1938	1emn		176	247	5.1e-12	0.07	-0.20		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1938	1emn		257	338	6.8e-09	0.05	-0.17		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1938	1fjs	L	65	108	3.4e-06	-0.01	0.03		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1938	1hcc		263	321	8.4e-11	0.63	0.88		GLYCOPROTEIN 16TH COMPLEMENT CONTROL	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN (/CCPS) OF FACTOR H 1HCC 3	
1938	1hcc		60	118	3.6e-10	0.52	0.18		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCPS) OF FACTOR H 1HCC 3	
1938	1qub	A	239	377	3.4e-09	0.37	-0.06		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N- GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1938	1qub	A	58	393	5.1e-24			94.07	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N- GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1938	1qub	A	61	355	5.1e-24	0.13	-0.19		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N- GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1938	1sfp		125	260	2.4e-27	0.55	0.24		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1938	1sfp		323	411	7.2e-09	-0.22	0.01		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1938	1spp	A	127	261	1.2e-27	0.42	0.06		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)
1938	1spp	A	325	411	6e-12	-0.06	0.17		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1938	1vvc		262	377	1.7e-09	0.37	0.35		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
1938	1vvc		264	353	2.4e-13	0.34	0.39		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
1938	1vvc		61	153	2.4e-10	0.30	0.13		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
1938	1vvc		61	186	3.4e-10	0.23	-0.12		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
1938	1xka	L	60	147	1.4e-08	0.19	-0.18		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GROWTH FACTOR LIKE DOMAIN
1939	1ckl	A	46	173	1.2e-22			50.88	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1939	1hcc		112	170	6e-11	0.91	0.82		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCPS) OF FACTOR H 1HCC 3	
1939	1hcc		113	170	8.5e-09	0.63	0.88		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCPS) OF FACTOR H 1HCC 3	
1939	1hfh		112	175	6e-10	0.96	0.98		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
1939	1hfi		109	171	1.7e-09	0.89	0.99		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
1939	1hfi		112	170	8e-11	0.42	0.89		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1	

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
1	972	1943	2710	784_1224
2	973			
3	974			
4	975			
5	976	1944	2711	784_852
6	977	1945	2712	787_7208
7	978	1946	2713	784_7010
8	979	1947	2714	784_3474
9	980	1948	2715	784_3474
10	981	1949	2716	784_8297
11	982	1950	2717	784_7231
12	983	1951	2718	784_8635
13	984	1952	2719	790_1453
14	985	1953	2720	784_9466
15	986	1954	2721	787_1547
16	987	1955	2722	784_1853
17	988	1956	2723	784_5326
18	989	1957	2724	784_3005
19	990	1958	2725	790_10069
20	991	1959	2726	784_2125
21	992	1960	2727	790_19500
22	993	1961	2728	784_1517
23	994	1962	2729	784_2106
24	995	1963	2730	789_2757
25	996	1964	2731	791_2477
26	997	1965	2732	784_6204
27	998			
28	999	1966	2733	784_5039
29	1000	1967	2734	790_9623
30	1001	1968	2735	784_6161
31	1002	1969	2736	784_3807
32	1003			
33	1004	1970	2737	785_2867
34	1005	1971	2738	784_1004
35	1006	1972	2739	784_1004
36	1007	1973	2740	784_6766
37	1008	1974	2741	787_5068
38	1009	1975	2742	788_13638
39	1010			
40	1011	1976	2743	784_7484
41	1012	1977	2744	788_4366
42	1013	1978	2745	787_3314
43	1014	1979	2746	784_5215
44	1015	1980	2747	784_4678
45	1016	1981	2748	788_12744
46	1017	1982	2749	788_12744
47	1018	1983	2750	789_2737
48	1019	1984	2751	790_20069

1128

Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
49	1020	1985	2752	789_5723
50	1021	1986	2753	784_9000
51	1022	1987	2754	784_5280
52	1023	1988	2755	789_6142
53	1024	1989	2756	788_7211
54	1025	1990	2757	784_897
55	1026	1991	2758	784_4500
56	1027	1992	2759	788_13656
57	1028	1993	2760	788_13656
58	1029	1994	2761	784_3451
59	1030	1995	2762	792_2255
60	1031	1996	2763	788_4373
61	1032	1997	2764	785_3219
62	1033	1998	2765	790_4641
63	1034			
64	1035	1999	2766	784_10172
65	1036	2000	2767	789_5937
66	1037	2001	2768	784_7576
67	1038			
68	1039	2002	2769	784_4621
69	1040	2003	2770	784_4621
70	1041	2004	2771	789_6210
71	1042	2005	2772	784_149
72	1043	2006	2773	789_5115
73	1044	2007	2774	789_5115
74	1045	2008	2775	789_5115
75	1046	2009	2776	784_4288
76	1047	2010	2777	790_19387
77	1048	2011	2778	790_783
78	1049			
79	1050	2012	2779	790_27924
80	1051	2013	2780	789_5641
81	1052	2014	2781	791_4242
82	1053			
83	1054	2015	2782	789_6305
84	1055	2016	2783	790_1497
85	1056			
86	1057	2017	2784	788_13665
87	1058	2018	2785	790_9974
88	1059	2019	2786	784_1994
89	1060	2020	2787	784_3267
90	1061	2021	2788	784_13
91	1062	2022	2789	784_1536
92	1063			
93	1064	2023	2790	784_4084
94	1065	2024	2791	784_6206
95	1066	2025	2792	785_1300
96	1067	2026	2793	787_7605
97	1068	2027	2794	785_2429

Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No. SEQ ID NO.) *
98	1069	2028	2795	784_4076
99	1070	2029	2796	784_10051
100	1071	2030	2797	784_9491
101	1072	2031	2798	784_4602
102	1073	2032	2799	784_2841
103	1074	2033	2800	787_249
104	1075			
105	1076	2034	2801	784_1700
106	1077	2035	2802	787_2626
107	1078	2036	2803	792_1911
108	1079	2037	2804	784_8811
109	1080	2038	2805	784_6218
110	1081	2039	2806	789_5846
111	1082	2040	2807	784_3634
112	1083	2041	2808	787_5208
113	1084	2042	2809	787_1179
114	1085	2043	2810	788_8383
115	1086	2044	2811	784_8836
116	1087	2045	2812	784_9029
117	1088	2046	2813	784_8770
118	1089	2047	2814	784_4083
119	1090	2048	2815	790_14642
120	1091	2049	2816	784_4420
121	1092	2050	2817	784_7113
122	1093			
123	1094	2051	2818	787_5474
124	1095	2052	2819	784_1582
125	1096			
126	1097	2053	2820	784_8765
127	1098	2054	2821	784_7761
128	1099	2055	2822	784_8791
129	1100	2056	2823	790_26782
130	1101	2057	2824	785_2423
131	1102	2058	2825	784_3090
132	1103	2059	2826	784_5080
133	1104			
134	1105	2060	2827	787_3785
135	1106	2061	2828	784_3091
136	1107	2062	2829	784_3091
137	1108			
138	1109	2063	2830	790_19641
139	1110			
140	1111	2064	2831	790_2500
141	1112	2065	2832	784_8758
142	1113	2066	2833	784_1076
143	1114	2067	2834	790_2608
144	1115	2068	2835	784_4358
145	1116	2069	2836	790_25033
146	1117	2070	2837	784_2446

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
147	1118	2071	2838	784_1044
148	1119	2072	2839	784_7636
149	1120	2073	2840	787_134
150	1121	2074	2841	791_2267
151	1122	2075	2842	784_774
152	1123	2076	2843	792_7564
153	1124	2077	2844	784_9970
154	1125			
155	1126	2078	2845	784_3910
156	1127			
157	1128	2079	2846	790_26952
158	1129	2080	2847	784_729
159	1130	2081	2848	784_8218
160	1131	2082	2849	784_8218
161	1132	2083	2850	784_4307
162	1133			
163	1134	2084	2851	790_1063
164	1135	2085	2852	784_9448
165	1136	2086	2853	790_308
166	1137	2087	2854	787_5972
167	1138	2088	2855	784_6680
168	1139			
169	1140			
170	1141	2089	2856	784_4742
171	1142	2090	2857	784_8152
172	1143	2091	2858	789_5276
173	1144	2092	2859	790_19423
174	1145	2093	2860	784_3231
175	1146			
176	1147	2094	2861	790_19135
177	1148	2095	2862	790_2859
178	1149			
179	1150	2096	2863	784_8713
180	1151	2097	2864	790_15184
181	1152	2098	2865	787_2134
182	1153	2099	2866	784_4938
183	1154			
184	1155	2100	2867	784_1071
185	1156	2101	2868	784_6181
186	1157	2102	2869	784_193
187	1158	2103	2870	790_24137
188	1159			
189	1160	2104	2871	787_5326
190	1161	2105	2872	784_1711
191	1162	2106	2873	784_7239
192	1163	2107	2874	784_3887
193	1164	2108	2875	787_10175
194	1165	2109	2876	792_6876
195	1166	2110	2877	790_17490

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
196	1167	2111	2878	788_12696
197	1168	2112	2879	784_183
198	1169	2113	2880	784_9962
199	1170	2114	2881	790_11346
200	1171	2115	2882	790_2375
201	1172	2116	2883	784_3218
202	1173	2117	2884	787_1179
203	1174	2118	2885	784_8095
204	1175	2119	2886	784_4778
205	1176	2120	2887	784_815
206	1177	2121	2888	792_633
207	1178	2122	2889	784_5858
208	1179	2123	2890	784_8485
209	1180	2124	2891	784_5325
210	1181	2125	2892	784_5417
211	1182	2126	2893	788_13391
212	1183	2127	2894	788_13391
213	1184	2128	2895	784_2249
214	1185	2129	2896	784_3755
215	1186	2130	2897	785_540
216	1187	2131	2898	787_5940
217	1188	2132	2899	787_7631
218	1189	2133	2900	791_4358
219	1190	2134	2901	784_4277
220	1191	2135	2902	787_10032
221	1192	2136	2903	784_1775
222	1193			
223	1194	2137	2904	784_2316
224	1195	2138	2905	784_7495
225	1196	2139	2906	784_7230
226	1197	2140	2907	784_5855
227	1198	2141	2908	785_828
228	1199	2142	2909	787_4973
229	1200	2143	2910	784_1993
230	1201	2144	2911	790_3164
231	1202	2145	2912	785_826
232	1203			
233	1204	2146	2913	784_4003
234	1205	2147	2914	788_12327
235	1206	2148	2915	784_8963
236	1207	2149	2916	785_3548
237	1208	2150	2917	784_2151
238	1209	2151	2918	789_629
239	1210	2152	2919	784_9496
240	1211	2153	2920	784_9496
241	1212	2154	2921	792_2014
242	1213			
243	1214			
244	1215			

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
245	1216	2155	2922	784_5314
246	1217	2156	2923	792_4190
247	1218	2157	2924	787_8011
248	1219	2158	2925	784_8794
249	1220	2159	2926	784_2261
250	1221	2160	2927	788_4268
251	1222	2161	2928	784_9684
252	1223	2162	2929	784_2368
253	1224	2163	2930	784_7928
254	1225	2164	2931	784_1856
255	1226	2165	2932	784_6106
256	1227	2166	2933	784_6106
257	1228	2167	2934	784_1626
258	1229	2168	2935	784_4080
259	1230	2169	2936	784_194
260	1231	2170	2937	787_7988
261	1232	2171	2938	784_4707
262	1233	2172	2939	789_2100
263	1234			
264	1235	2173	2940	784_893
265	1236	2174	2941	789_1598
266	1237	2175	2942	784_834
267	1238	2176	2943	787_6026
268	1239			
269	1240	2177	2944	787_10200
270	1241	2178	2945	784_8799
271	1242	2179	2946	784_8340
272	1243	2180	2947	784_989
273	1244	2181	2948	788_5199
274	1245			
275	1246	2182	2949	787_6215
276	1247	2183	2950	784_2499
277	1248	2184	2951	784_3930
278	1249	2185	2952	784_3769
279	1250	2186	2953	784_2094
280	1251	2187	2954	785_1035
281	1252			
282	1253	2188	2955	784_9552
283	1254	2189	2956	784_9552
284	1255	2190	2957	790_21775
285	1256	2191	2958	785_3564
286	1257	2192	2959	784_1049
287	1258	2193	2960	790_19814
288	1259	2194	2961	784_1922
289	1260	2195	2962	784_4381
290	1261	2196	2963	784_1957
291	1262	2197	2964	787_5835
292	1263	2198	2965	787_5552
293	1264	2199	2966	784_9381

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
294	1265			
295	1266	2200	2967	788 10351
296	1267	2201	2968	784 6729
297	1268	2202	2969	784 2524
298	1269	2203	2970	784 9087
299	1270	2204	2971	788 13641
300	1271	2205	2972	792 4273
301	1272	2206	2973	784 8150
302	1273	2207	2974	784 2159
303	1274	2208	2975	784 9338
304	1275			
305	1276	2209	2976	784 7665
306	1277	2210	2977	784 2015
307	1278	2211	2978	787 9885
308	1279	2212	2979	790 14080
309	1280	2213	2980	784 3052
310	1281			
311	1282	2214	2981	784 1386
312	1283	2215	2982	792 273
313	1284			
314	1285			
315	1286	2216	2983	792 6952
316	1287	2217	2984	784 3783
317	1288	2218	2985	784 3783
318	1289			
319	1290	2219	2986	790 1199
320	1291	2220	2987	792 5495
321	1292	2221	2988	784 2270
322	1293	2222	2989	784 1824
323	1294	2223	2990	787 5550
324	1295	2224	2991	790 27374
325	1296			
326	1297	2225	2992	790 14323
327	1298			
328	1299			
329	1300	2226	2993	784 8128
330	1301	2227	2994	784 9591
331	1302	2228	2995	784 7674
332	1303	2229	2996	784 3111
333	1304	2230	2997	790 22977
334	1305	2231	2998	784 1073
335	1306	2232	2999	784 636
336	1307	2233	3000	784 6892
337	1308	2234	3001	789 658
338	1309	2235	3002	790 2458
339	1310	2236	3003	792 4252
340	1311	2237	3004	787 10241
341	1312	2238	3005	784 4656
342	1313	2239	3006	784 7738

Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
343	1314			
344	1315	2240	3007	784_3494
345	1316	2241	3008	784_7572
346	1317	2242	3009	784_2401
347	1318	2243	3010	787_2452
348	1319	2244	3011	784_9487
349	1320	2245	3012	784_2664
350	1321			
351	1322	2246	3013	787_7317
352	1323	2247	3014	790_10590
353	1324	2248	3015	789_4906
354	1325			
355	1326	2249	3016	784_10280
356	1327	2250	3017	787_2292
357	1328	2251	3018	785_364
358	1329	2252	3019	784_4447
359	1330	2253	3020	787_8910
360	1331	2254	3021	784_9704
361	1332			
362	1333	2255	3022	784_2063
363	1334	2256	3023	784_1972
364	1335	2257	3024	784_6431
365	1336	2258	3025	784_6001
366	1337	2259	3026	784_6950
367	1338	2260	3027	790_5583
368	1339	2261	3028	784_1305
369	1340	2262	3029	790_5747
370	1341	2263	3030	784_6493
371	1342			
372	1343	2264	3031	790_14586
373	1344	2265	3032	787_2133
374	1345			
375	1346	2266	3033	788_4349
376	1347	2267	3034	787_10237
377	1348			
378	1349	2268	3035	784_254
379	1350			
380	1351	2269	3036	784_5321
381	1352	2270	3037	791_1515
382	1353	2271	3038	787_9061
383	1354	2272	3039	784_7513
384	1355	2273	3040	787_3196
385	1356	2274	3041	788_13324
386	1357			
387	1358			
388	1359	2275	3042	784_2074
389	1360	2276	3043	787_5928
390	1361	2277	3044	784_2322
391	1362	2278	3045	790_12083

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No. SEQ ID NO.) *
392	1363	2279	3046	784 4511
393	1364	2280	3047	790 1886
394	1365			
395	1366	2281	3048	784 232
396	1367	2282	3049	784 1884
397	1368			
398	1369	2283	3050	784 2082
399	1370	2284	3051	790 24248
400	1371	2285	3052	784 3847
401	1372	2286	3053	790 21352
402	1373			
403	1374	2287	3054	787 7127
404	1375	2288	3055	784 5344
405	1376	2289	3056	787 10040
406	1377	2290	3057	790 15388
407	1378	2291	3058	784 2116
408	1379	2292	3059	784 10202
409	1380			
410	1381	2293	3060	784 5329
411	1382	2294	3061	784 5329
412	1383	2295	3062	784 5329
413	1384	2296	3063	784 1921
414	1385	2297	3064	784 8888
415	1386	2298	3065	784 6518
416	1387	2299	3066	788 5134
417	1388			
418	1389	2300	3067	789 439
419	1390			
420	1391	2301	3068	784 2147
421	1392	2302	3069	787 8778
422	1393	2303	3070	790 2428
423	1394			
424	1395	2304	3071	787 1365
425	1396	2305	3072	790 15951
426	1397	2306	3073	784 9724
427	1398			
428	1399			
429	1400			
430	1401	2307	3074	790 16631
431	1402	2308	3075	790 1660
432	1403	2309	3076	787 1694
433	1404	2310	3077	790 9736
434	1405	2311	3078	790 19371
435	1406			
436	1407			
437	1408	2312	3079	784 5732
438	1409	2313	3080	790 28173
439	1410	2314	3081	787 8248
440	1411	2315	3082	787 7219

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
441	1412	2316	3083	791_634
442	1413	2317	3084	791_401
443	1414	2318	3085	784_5558
444	1415	2319	3086	784_2037
445	1416			
446	1417	2320	3087	784_10005
447	1418	2321	3088	784_10064
448	1419	2322	3089	784_10064
449	1420	2323	3090	787_10073
450	1421	2324	3091	789_644
451	1422	2325	3092	784_2292
452	1423			
453	1424	2326	3093	784_9391
454	1425	2327	3094	787_9807
455	1426	2328	3095	784_8920
456	1427			
457	1428	2329	3096	784_4699
458	1429			
459	1430	2330	3097	784_908
460	1431	2331	3098	787_5515
461	1432	2332	3099	787_7919
462	1433	2333	3100	789_2723
463	1434	2334	3101	784_1807
464	1435	2335	3102	790_8144
465	1436	2336	3103	784_9640
466	1437	2337	3104	787_5310
467	1438	2338	3105	790_11190
468	1439	2339	3106	787_9200
469	1440	2340	3107	790_15075
470	1441	2341	3108	784_531
471	1442	2342	3109	792_7587
472	1443	2343	3110	784_10061
473	1444	2344	3111	790_3597
474	1445			
475	1446	2345	3112	787_161
476	1447			
477	1448			
478	1449	2346	3113	790_11842
479	1450	2347	3114	784_5654
480	1451	2348	3115	787_3486
481	1452	2349	3116	792_7587
482	1453	2350	3117	784_8992
483	1454	2351	3118	784_4957
484	1455			
485	1456	2352	3119	790_1917
486	1457			
487	1458			
488	1459	2353	3120	787_3947
489	1460	2354	3121	784_6581

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
490	1461			
491	1462	2355	3122	784_1691
492	1463			
493	1464	2356	3123	790_15794
494	1465	2357	3124	784_3609
495	1466	2358	3125	787_4906
496	1467	2359	3126	790_1952
497	1468	2360	3127	790_3855
498	1469	2361	3128	787_4361
499	1470	2362	3129	787_2551
500	1471			
501	1472	2363	3130	788_3778
502	1473	2364	3131	790_29526
503	1474	2365	3132	784_10066
504	1475	2366	3133	784_10066
505	1476	2367	3134	787_9841
506	1477	2368	3135	787_2410
507	1478	2369	3136	790_12704
508	1479			
509	1480	2370	3137	790_6209
510	1481	2371	3138	789_3411
511	1482	2372	3139	784_9888
512	1483	2373	3140	790_29516
513	1484			
514	1485	2374	3141	784_6670
515	1486	2375	3142	785_555
516	1487	2376	3143	790_10968
517	1488	2377	3144	787_5633
518	1489	2378	3145	784_9133
519	1490	2379	3146	784_6391
520	1491			
521	1492	2380	3147	787_6115
522	1493	2381	3148	784_2126
523	1494	2382	3149	784_8754
524	1495	2383	3150	790_14360
525	1496	2384	3151	787_9248
526	1497	2385	3152	787_4445
527	1498	2386	3153	787_5648
528	1499	2387	3154	790_22816
529	1500			
530	1501			
531	1502	2388	3155	788_9557
532	1503	2389	3156	784_7364
533	1504	2390	3157	787_10184
534	1505	2391	3158	790_1148
535	1506			
536	1507	2392	3159	788_5424
537	1508	2393	3160	787_10099
538	1509			

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No. SEQ ID NO.) *
539	1510			
540	1511			
541	1512	2394	3161	784_10185
542	1513	2395	3162	784_3322
543	1514	2396	3163	784_1553
544	1515	2397	3164	790_19723
545	1516			
546	1517	2398	3165	787_813
547	1518	2399	3166	790_16130
548	1519	2400	3167	784_972
549	1520	2401	3168	790_23073
550	1521	2402	3169	784_5293
551	1522	2403	3170	784_3041
552	1523	2404	3171	784_5365
553	1524	2405	3172	790_11131
554	1525	2406	3173	787_3748
555	1526	2407	3174	789_4975
556	1527	2408	3175	787_3743
557	1528	2409	3176	787_3743
558	1529			
559	1530	2410	3177	787_2855
560	1531	2411	3178	787_2447
561	1532	2412	3179	784_9156
562	1533			
563	1534	2413	3180	784_7447
564	1535	2414	3181	784_7447
565	1536	2415	3182	790_18202
566	1537	2416	3183	789_1599
567	1538	2417	3184	784_4033
568	1539	2418	3185	784_5329
569	1540	2419	3186	790_10614
570	1541	2420	3187	784_5434
571	1542	2421	3188	784_9815
572	1543	2422	3189	787_2513
573	1544			
574	1545			
575	1546	2423	3190	784_5038
576	1547	2424	3191	784_1339
577	1548	2425	3192	784_3599
578	1549			
579	1550	2426	3193	790_12410
580	1551			
581	1552			
582	1553			
583	1554	2427	3194	784_1927
584	1555	2428	3195	790_26548
585	1556	2429	3196	790_7287
586	1557	2430	3197	790_7287
587	1558	2431	3198	790_15680

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
588	1559	2432	3199	784_1045
589	1560	2433	3200	790_6409
590	1561	2434	3201	787_2322
591	1562			
592	1563	2435	3202	784_8245
593	1564	2436	3203	784_8245
594	1565	2437	3204	790_15575
595	1566			
596	1567			
597	1568			
598	1569	2438	3205	784_7955
599	1570	2439	3206	787_2691
600	1571	2440	3207	787_5853
601	1572	2441	3208	787_10136
602	1573	2442	3209	784_8360
603	1574	2443	3210	790_22260
604	1575			
605	1576	2444	3211	784_2677
606	1577	2445	3212	784_8042
607	1578	2446	3213	789_6361
608	1579	2447	3214	784_5150
609	1580			
610	1581			
611	1582	2448	3215	784_3279
612	1583			
613	1584	2449	3216	790_28630
614	1585	2450	3217	784_1238
615	1586	2451	3218	787_9483
616	1587	2452	3219	787_4499
617	1588			
618	1589			
619	1590	2453	3220	790_2304
620	1591	2454	3221	791_1303
621	1592	2455	3222	791_1303
622	1593			
623	1594	2456	3223	790_16004
624	1595			
625	1596	2457	3224	790_11182
626	1597	2458	3225	784_1981
627	1598			
628	1599			
629	1600	2459	3226	784_1026
630	1601			
631	1602	2460	3227	790_16240
632	1603	2461	3228	790_14734
633	1604			
634	1605			
635	1606	2462	3229	784_9753
636	1607	2463	3230	789_5821

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
637	1608			
638	1609			
639	1610	2464	3231	788_2614
640	1611			
641	1612	2465	3232	784_4769
642	1613	2466	3233	784_4769
643	1614	2467	3234	784_2968
644	1615	2468	3235	784_142
645	1616	2469	3236	784_5903
646	1617	2470	3237	784_7930
647	1618			
648	1619	2471	3238	784_3247
649	1620	2472	3239	784_3247
650	1621	2473	3240	787_2820
651	1622	2474	3241	784_10030
652	1623	2475	3242	784_10050
653	1624	2476	3243	784_1136
654	1625	2477	3244	790_3151
655	1626	2478	3245	784_4242
656	1627	2479	3246	791_4309
657	1628	2480	3247	790_3196
658	1629	2481	3248	790_28262
659	1630	2482	3249	784_3774
660	1631	2483	3250	784_1361
661	1632			
662	1633	2484	3251	784_5612
663	1634	2485	3252	784_3593
664	1635			
665	1636	2486	3253	789_1613
666	1637			
667	1638			
668	1639	2487	3254	790_25912
669	1640	2488	3255	787_10217
670	1641	2489	3256	784_6584
671	1642	2490	3257	784_5348
672	1643	2491	3258	785_1029
673	1644	2492	3259	784_1517
674	1645			
675	1646	2493	3260	787_766
676	1647	2494	3261	784_10155
677	1648	2495	3262	790_26542
678	1649	2496	3263	787_5996
679	1650			
680	1651	2497	3264	785_3492
681	1652	2498	3265	784_5074
682	1653	2499	3266	787_10214
683	1654	2500	3267	784_5399
684	1655			
685	1656	2501	3268	784_3782

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No. SEQ ID NO.) *
686	1657			
687	1658	2502	3269	790_15978
688	1659	2503	3270	790_11139
689	1660	2504	3271	784_2833
690	1661	2505	3272	787_4050
691	1662	2506	3273	787_6078
692	1663			
693	1664	2507	3274	790_3691
694	1665			
695	1666	2508	3275	784_2305
696	1667	2509	3276	784_2305
697	1668	2510	3277	790_195
698	1669	2511	3278	784_3569
699	1670			
700	1671			
701	1672	2512	3279	785_3128
702	1673	2513	3280	788_12134
703	1674			
704	1675	2514	3281	787_1910
705	1676	2515	3282	784_6986
706	1677	2516	3283	792_6424
707	1678	2517	3284	789_6251
708	1679	2518	3285	790_16758
709	1680	2519	3286	784_1388
710	1681	2520	3287	790_12927
711	1682			
712	1683	2521	3288	784_5409
713	1684			
714	1685			
715	1686	2522	3289	789_6307
716	1687	2523	3290	789_6307
717	1688	2524	3291	789_5195
718	1689	2525	3292	784_3617
719	1690	2526	3293	789_4172
720	1691	2527	3294	790_15081
721	1692	2528	3295	789_4177
722	1693	2529	3296	789_2661
723	1694	2530	3297	789_1635
724	1695	2531	3298	788_8352
725	1696	2532	3299	787_9506
726	1697	2533	3300	784_7635
727	1698	2534	3301	788_9560
728	1699	2535	3302	788_12695
729	1700	2536	3303	784_691
730	1701	2537	3304	784_8513
731	1702	2538	3305	784_5838
732	1703	2539	3306	784_9765
733	1704			
734	1705	2540	3307	784_7285

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
735	1706			
736	1707	2541	3308	787_2751
737	1708	2542	3309	787_930
738	1709	2543	3310	784_4990
739	1710	2544	3311	784_4990
740	1711	2545	3312	788_9526
741	1712	2546	3313	788_9526
742	1713	2547	3314	788_9526
743	1714	2548	3315	787_3379
744	1715	2549	3316	784_3729
745	1716	2550	3317	789_657
746	1717	2551	3318	784_2162
747	1718	2552	3319	787_3728
748	1719	2553	3320	791_2939
749	1720	2554	3321	787_6837
750	1721	2555	3322	784_5899
751	1722			
752	1723			
753	1724			
754	1725			
755	1726	2556	3323	790_4177
756	1727			
757	1728	2557	3324	784_10284
758	1729	2558	3325	787_2826
759	1730			
760	1731	2559	3326	784_4266
761	1732	2560	3327	790_13065
762	1733			
763	1734	2561	3328	790_3689
764	1735			
765	1736			
766	1737			
767	1738			
768	1739	2562	3329	787_134
769	1740			
770	1741	2563	3330	790_5571
771	1742	2564	3331	790_29586
772	1743	2565	3332	790_795
773	1744	2566	3333	784_9909
774	1745	2567	3334	790_6056
775	1746	2568	3335	787_2295
776	1747			
777	1748			
778	1749			
779	1750	2569	3336	791_1055
780	1751			
781	1752			
782	1753			
783	1754	2570	3337	784_2972

Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
784	1755	2571	3338	790_421
785	1756	2572	3339	784_9071
786	1757	2573	3340	784_9071
787	1758	2574	3341	784_2812
788	1759			
789	1760	2575	3342	784_8343
790	1761	2576	3343	790_24179
791	1762	2577	3344	787_5796
792	1763			
793	1764			
794	1765	2578	3345	787_2186
795	1766	2579	3346	784_3425
796	1767	2580	3347	784_2450
797	1768	2581	3348	790_10545
798	1769	2582	3349	787_10022
799	1770	2583	3350	792_7526
800	1771	2584	3351	788_6854
801	1772			
802	1773			
803	1774			
804	1775			
805	1776			
806	1777	2585	3352	790_11591
807	1778			
808	1779			
809	1780			
810	1781			
811	1782	2586	3353	790_17425
812	1783	2587	3354	787_5611
813	1784	2588	3355	790_23540
814	1785			
815	1786	2589	3356	784_5005
816	1787	2590	3357	788_6661
817	1788			
818	1789	2591	3358	790_29528
819	1790	2592	3359	784_7697
820	1791			
821	1792			
822	1793	2593	3360	787_3303
823	1794			
824	1795	2594	3361	785_2074
825	1796	2595	3362	792_4185
826	1797			
827	1798	2596	3363	784_3696
828	1799	2597	3364	784_5320
829	1800	2598	3365	784_4959
830	1801	2599	3366	787_3489
831	1802	2600	3367	790_20040
832	1803	2601	3368	784_9839

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
833	1804			
834	1805			
835	1806			
836	1807	2602	3369	788_13648
837	1808			
838	1809	2603	3370	790_17373
839	1810			
840	1811	2604	3371	784_8575
841	1812			
842	1813			
843	1814	2605	3372	787_10247
844	1815	2606	3373	787_3385
845	1816			
846	1817			
847	1818			
848	1819	2607	3374	789_6391
849	1820	2608	3375	784_8632
850	1821	2609	3376	784_1619
851	1822			
852	1823	2610	3377	788_8284
853	1824	2611	3378	787_1648
854	1825	2612	3379	784_8333
855	1826	2613	3380	790_13448
856	1827	2614	3381	790_27871
857	1828	2615	3382	790_11655
858	1829	2616	3383	790_17178
859	1830			
860	1831	2617	3384	787_10232
861	1832	2618	3385	784_6099
862	1833			
863	1834	2619	3386	790_19908
864	1835	2620	3387	784_603
865	1836	2621	3388	784_603
866	1837	2622	3389	790_27344
867	1838			
868	1839	2623	3390	784_10006
869	1840	2624	3391	784_10006
870	1841	2625	3392	784_10006
871	1842	2626	3393	784_10006
872	1843			
873	1844	2627	3394	790_4164
874	1845	2628	3395	784_2160
875	1846	2629	3396	784_2491
876	1847	2630	3397	792_2758
877	1848	2631	3398	790_26542
878	1849	2632	3399	790_15426
879	1850	2633	3400	784_5086
880	1851	2634	3401	784_5696
881	1852	2635	3402	784_9484

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Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No., SEQ ID NO.) *
882	1853	2636	3403	784_8961
883	1854			
884	1855	2637	3404	784_1073
885	1856	2638	3405	787_9241
886	1857	2639	3406	784_3613
887	1858	2640	3407	784_3481
888	1859	2641	3408	792_1019
889	1860	2642	3409	790_20139
890	1861	2643	3410	784_7697
891	1862	2644	3411	790_669
892	1863			
893	1864			
894	1865	2645	3412	784_9086
895	1866	2646	3413	785_610
896	1867	2647	3414	784_382
897	1868	2648	3415	790_436
898	1869	2649	3416	789_350
899	1870	2650	3417	784_221
900	1871			
901	1872			
902	1873	2651	3418	784_1121
903	1874	2652	3419	784_3651
904	1875	2653	3420	784_1084
905	1876	2654	3421	784_3935
906	1877	2655	3422	784_7140
907	1878	2656	3423	784_4580
908	1879	2657	3424	790_12684
909	1880	2658	3425	784_9819
910	1881	2659	3426	784_454
911	1882	2660	3427	791_3463
912	1883	2661	3428	790_13539
913	1884	2662	3429	790_85
914	1885	2663	3430	790_29490
915	1886	2664	3431	787_2532
916	1887	2665	3432	791_2376
917	1888	2666	3433	784_1870
918	1889	2667	3434	784_9111
919	1890	2668	3435	784_2245
920	1891	2669	3436	784_9212
921	1892	2670	3437	784_2900
922	1893			
923	1894			
924	1895	2671	3438	787_3438
925	1896	2672	3439	787_4767
926	1897	2673	3440	787_4767
927	1898	2674	3441	787_2408
928	1899	2675	3442	791_311
929	1900			
930	1901			

Table 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
931	1902	2676	3443	787_233
932	1903			
933	1904	2677	3444	787_4124
934	1905	2678	3445	787_4124
935	1906	2679	3446	791_1604
936	1907			
937	1908	2680	3447	784_1468
938	1909	2681	3448	787_1602
939	1910	2682	3449	784_6971
940	1911	2683	3450	784_9131
941	1912	2684	3451	788_1717
942	1913	2685	3452	787_2644
943	1914	2686	3453	784_4755
944	1915	2687	3454	784_5576
945	1916	2688	3455	784_5576
946	1917	2689	3456	787_8607
947	1918			
948	1919			
949	1920	2690	3457	784_3786
950	1921	2691	3458	790_6872
951	1922	2692	3459	784_5341
952	1923	2693	3460	788_7215
953	1924	2694	3461	790_23518
954	1925	2695	3462	784_668
955	1926	2696	3463	787_7442
956	1927	2697	3464	784_2563
957	1928	2698	3465	784_10090
958	1929	2699	3466	787_1110
959	1930	2700	3467	784_2417
960	1931			
961	1932	2701	3468	784_1346
962	1933	2702	3469	784_2272
963	1934	2703	3470	784_4173
964	1935	2704	3471	784_9318
965	1936	2705	3472	784_5363
966	1937	2706	3473	784_4084
967	1938			
968	1939			
969	1940	2707	3474	790_4256
970	1941	2708	3475	784_446
971	1942	2709	3476	790_11491

*784_XXX = SEQ ID NO: XXX of Attorney Docket No. 784, US Serial No. 09/488,725 filed 01/21/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

785_XXX = SEQ ID NO: XXX of Attorney Docket No. 785, US Serial No. 09/491,404 filed 01/25/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

Table 6

787_XXX = SEQ ID NO: XXX of Attorney Docket No. 787, US Serial No. 09/496,914 filed 02/03/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

788_XXX = SEQ ID NO: XXX of Attorney Docket No. 788, US Serial No. 09/515,126 filed 02/28/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

789_XXX = SEQ ID NO: XXX of Attorney Docket No. 789, US Serial No. 09/519,705 filed 03/07/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

790_XXX = SEQ ID NO: XXX of Attorney Docket No. 790, US Serial No. 09/540,217 filed 03/31/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

791_XXX = SEQ ID NO: XXX of Attorney Docket No. 791, US Serial No. 09/552,929 filed 04/18/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

792_XXX = SEQ ID NO: XXX of Attorney Docket No. 792, US Serial No. 09/577,408 filed 05/18/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

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Table 7

SEQ ID	Chromosomal location
1	16
2	6q23
3	6q23
4	6q23
5	7q31
6	5
7	11q12
8	4
9	4
10	1
11	18
12	15q26
13	14
14	12
15	5
16	Xp11.1-11.3
17	11q14
18	6q21.
19	11
20	16
23	16
24	10q24-q25
25	18
26	17
27	Xp11.21-11.3.
28	16
29	8
30	10
31	6
32	12
33	3p24.3
34	17
35	17
36	4
38	1p32.2-34.2
39	9
40	10
41	17
42	1
43	20p11.23-20p11.22
44	2
47	2
48	21
49	20
50	3
51	14
52	6p21.2-21.31.
54	19
55	15q11.1
56	12pter-p13.31
57	12pter-p13.31
58	20
59	17q24-q25
60	9
61	17

1149

Table 7

SEQ ID	Chromosomal location
62	6q14.3-16.2
63	17
64	16
65	12p13
66	1p36.11-36.2.
67	6q23
70	19q13.4
71	9q32-33.2
72	6p12.2
73	6p12.2
74	6p12.2
76	15q15.3
77	20
79	11pter-p15.5
80	9
81	2q37
83	4
84	8
85	17
86	16
87	5p15.2-q12.3
90	19
91	20
92	13
94	17
95	12
96	6q14.2-16.1
97	18
98	15q21.3
99	17
100	2
101	17
102	19
103	6
104	7q36
105	20.
106	4
108	11q13
109	16
110	19
111	3
114	19
115	17
116	16
117	19
118	5
122	6p12.3-21.2
123	9
124	3
126	1q21.2-q22
127	11
128	15
129	15
130	6p12.2-21.1
131	2

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Table 7

SEQ ID	Chromosomal location
132	10
135	20q11.2-q12
136	20q11.2-q12
137	18q11
138	11q22.3-q23
140	2p23.3-q34
142	19
143	15
144	8
145	16q24.1
146	17
149	16
150	10
151	17
152	19
153	16p12
157	20p11.21-11.23.
159	13
160	13
163	5
164	X
165	11
166	9
167	1
169	1
170	17
171	6p21.3
172	15q13
173	17
174	3
175	12
177	19p13.2
179	5
180	9
181	17
182	22q13.1-13.2
184	17
185	15
186	3
187	8q24-qter
188	3
189	4q22-q24
190	19
191	18p11.3
192	19
193	11
195	4
196	6
198	19
199	4
200	Xq28
201	19
203	2
205	19
207	17

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Table 7

SEQ ID	Chromosomal location
208	15
209	1p36.11-36.23
214	2
215	3
216	3
217	22q13.1.
218	12
219	14
220	9q34.1
222	17q21
223	19
224	8
225	18
226	1
228	11q
229	4
230	8
231	6
235	19
236	4
237	20
238	17
239	5
240	5
243	19
244	11
246	3
247	10
248	5
249	11
250	19
251	15
253	4
254	18
255	9
256	9
257	11
258	1
259	10
261	1
262	6
264	5p14.3-q15
268	6
269	18p11.3
270	8
271	1q42.11-42.3
272	3
273	2
275	X
276	15
278	3
279	X
280	7q33
282	3
283	3

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Table 7

SEQ ID	Chromosomal location
284	15
286	7
287	5
288	9q34.11-34.13
290	15
291	14q21
292	15q21.3
293	19
294	16
296	12
297	19
298	14q24.3
299	20p11
300	18p11.2
00001262Fb231	
301	3
304	9p12-13.3
305	17
306	6
308	20
309	16
310	18
311	4q26-q27
312	5
314	8p23
315	11
316	3
317	3
318	1q22-q23
319	22q12.3-13.2
320	13q12.11-12.3
321	7
323	11
324	18
325	1
327	6q22.1-6q22.33
328	9
329	5
331	5
332	8
334	12q
336	9
337	19
338	5
339	15
340	3q
341	13
342	18
343	1p31.2-32.2
344	2
345	17
346	11q14
347	19q13.13-q13.2
348	19
349	3

1153

Table 7

SEQ ID	Chromosomal location
350	17
351	14
352	19q13.4
353	8q
354	14
356	16
357	18q12
358	17q11
359	Xp11.1-11.3
360	4
362	19
363	17
364	11q22
365	19
366	15
367	5
369	21q22.2D21S349-MX1
370	8
371	3p
373	19
374	8q24.1-q24.2
375	16
377	17
378	16
380	17
381	1
382	16
383	19
384	Xq22.1-23
385	5p
386	X
387	19
388	4p16
389	8
391	21q22.3
392	11
393	19
396	19
398	19
400	1q32
402	13q34
403	X
404	16
406	5
407	18
409	3
410	1
411	1
412	1
413	7
414	19q13.3-q13.4
415	6
416	9
417	14
418	1

1154

Table 7

SEQ ID	Chromosomal location
419	10
421	5
422	02
423	8p22
424	11
425	6q12-13
426	19q13.43
427	X
428	6
429	5
430	20
00001814Fc201	
431	11
433	19
434	12q
436	4q28
437	15
438	12
440	1
441	5q
442	6p12.3-21.2
443	7q35
446	11q13
447	X
448	X
449	14q24.3
452	17q12-q21
455	17
456	4
457	7
459	18q11.2
463	5
464	22q12
465	5
467	15
468	19
469	2
471	20
473	unknown
474	17
475	2
476	17
477	17
478	20p12.3-13.
479	17
480	19
481	20
483	19
486	15q15
487	10p12.1-p11.1
490	5q35
491	19
492	16p13.3
493	16p13.3
494	17

1155

Table 7

SEQ ID	Chromosomal location
495	8
496	3
497	11q23
498	3
499	15
500	19
501	11
502	11q14
503	17
504	17
506	17
507	19
508	2q36
509	20q11.21-13.13
510	19
511	Xp11.1-11.22
512	5
513	6
514	6p24.1-25.3
515	12q
516	22
518	17
519	18
521	10q21
523	5
524	8
00002205Fg041	
525	8
526	2q31
527	17
528	16
529	4q22-q24
530	22q12.3
531	18
532	18
534	10
536	6
539	1p33-34.3
540	10
541	2
542	10
543	5
544	4
545	12
546	17
547	16
548	18
551	16
552	16
553	17
554	Xq13.2-21.1
558	8
559	Xq13.3-21.2
560	11
561	16q24.3

1156

Table 7

SEQ ID	Chromosomal location
562	17
563	11
564	11
565	10
566	X
567	13q32.21-33.3
568	11
569	20q11.21-q11.23
571	X
572	2p13
573	20
574	10
576	6q25.2-26
579	20
580	17
581	14q24.3
582	X
583	6p21-p12
584	11q22
588	16
589	2
590	16p13.3
591	17
592	5
593	5
594	21q22.2
596	1p13.1-13.3
597	17
598	Xp11.4-21.2
599	1p34.1-36.11
601	12
602	11
603	14q21.1-q21.3
604	11cen-q12.3
605	3
606	11
608	17
609	13q22.1-31.1
610	5
611	17
613	13
614	3
616	11
617	5
620	1q23-25.
621	1q23-25.
622	17
623	15
624	15
625	11
626	14
627	17
628	12
632	6p12.1-21.1
633	19q13.4

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Table 7

SEQ ID	Chromosomal location
634	4
635	5
637	9p13.1-13.3
638	17p11.2
639	Xq22.1-22.3
640	20q13.3
641	1p22.3-31.2
642	1p22.3-31.2
643	10
644	9q21.2-22.1
645	1
646	10q23-q24
648	8
649	8
650	16
651	17pter-p13.1
652	19
653	X
654	17
655	9
656	1
657	18
658	22
659	11
661	15
663	12
664	5
665	19
666	Xq13.1-21.1.
667	10
668	4
669	17q21.33
670	15q15
671	4q28
672	6
673	15
674	19
675	2
676	19
679	6
681	22
682	11q14
683	15
685	Xp11.21-11.23
686	3
687	19
688	11
689	20
691	16q21
692	3
693	9
694	10
695	2
696	2
697	17

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Table 7

SEQ ID	Chromosomal location
698	11p14
699	3q
700	8p21-p12
701	19
702	19
703	22
704	8p23-p22
705	19
708	5
710	17
711	4
712	X
713	1q41-q42
714	3
715	1
716	1
717	18
718	12
721	6p21.3-22.2
722	13
724	6
725	13q14
727	20
729	20q11.21-13.13
730	16
731	16
732	17
733	2
734	15
735	16
737	15
738	15
739	15
740	6q25.2-26
741	6q25.2-26
742	6q25.2-26
743	4
744	9q34
745	11q13
746	12
749	20p11.1-11.22
751	9
752	5q31-q32
753	2
754	2
755	19p11-q11
758	18
760	16
761	10q23.3
763	9
764	13q22.1-31.1
765	14q23-q24
766	1
767	1
768	16

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Table 7

SEQ ID	Chromosomal location
769	11
770	9
773	3
775	13
776	1
777	12p13
779	17
782	14
784	17
785	20q11.22-12
786	20q11.22-12
787	5
788	8
790	6q22.1-22.33
791	5
792	13
793	7
794	20p11.21-11.23
795	6q14.1-15
796	16
797	9p13.1-13.3
798	2
799	15q21.3
800	5q
801	8
802	8
803	3p
805	10
806	2
807	17q21-q22
808	18q21
809	11
811	2
813	13
814	11p13
815	12
817	10
818	2
820	18
822	3
823	9
824	3
826	8q
828	20
829	11q23
830	19
831	1
836	17
838	1
839	17
840	22q13.1
841	5
842	1
843	3
844	19q12

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Table 7

SEQ ID	Chromosomal location
845	19
846	10
847	16
848	9
849	3
850	10
851	15q21.2
852	8
854	15q21.3
855	4
856	1
857	5
858	3
860	19q13.2
861	20q11.2-12
862	8
863	X
864	3
865	3
866	10
867	9
868	11
869	11
870	11
871	11
872	7
874	17
875	2
876	10
878	2q14-q21
879	12
880	19
881	8q13
882	8
883	17p13.3
884	12q
885	3
886	18
887	12
888	3p21.1-q13.13
889	19
891	Xp11.23-11.4
892	4
893	1
894	X
895	Xq22.2-23
896	19
897	3
898	4
899	19
900	19
901	9
902	19
903	8
904	18

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Table 7

SEQ ID	Chromosomal location
908	12q
909	19
910	9
911	8
912	12q23-q24
913	6
914	19
915	1p36.11-36.33
916	17
917	19
918	11q
919	19
99990980Ff202	
920	19
99990980Ff202	
921	3q
924	5
925	5
926	5
927	19
928	12q13
932	20
933	2p12-q11
934	2p12-q11
935	2p12-q11
937	7
939	16
940	6p11.2-q12.
941	3
943	10
944	22q11.2
945	22q11.2
946	9q31.3-33.3
949	2p13
950	17
952	1
954	22q12.3-13.2
955	16
956	17
957	17
958	19
959	19
960	4
962	17p11.2
963	Xq21.31-22.1
964	16
966	19
967	1p34.1-36.11
968	1p34.1-36.11
970	6p12.3-21.2
971	19q13.4

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
1	972	1
2	973	2
3	974	3
4	975	4
5	976	5
6	977	6
7	978	7
8	979	9
9	980	10
10	981	11
11	982	12
12	983	13
13	984	14
14	985	15
15	986	16
16	987	17
17	988	18
18	989	19
19	990	20
20	991	21
21	992	22
22	993	23
23	994	24
24	995	25
25	996	26
26	997	27
27	998	28
28	999	29
29	1000	30
30	1001	31
31	1002	32
32	1003	33
33	1004	34
34	1005	35
35	1006	36
36	1007	37
37	1008	38
38	1009	39
39	1010	40
40	1011	41
41	1012	42
42	1013	43
43	1014	44
44	1015	45
45	1016	46
46	1017	47
47	1018	48
48	1019	49
49	1020	50
50	1021	51
51	1022	52
52	1023	53

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
53	1024	54
54	1025	55
55	1026	56
56	1027	57
57	1028	58
58	1029	59
59	1030	60
60	1031	61
61	1032	62
62	1033	63
63	1034	64
64	1035	65
65	1036	66
66	1037	67
67	1038	68
68	1039	69
69	1040	70
70	1041	71
71	1042	72
72	1043	73
73	1044	74
74	1045	75
75	1046	76
76	1047	77
77	1048	78
78	1049	79
79	1050	80
80	1051	81
81	1052	82
82	1053	83
83	1054	84
84	1055	85
85	1056	86
86	1057	87
87	1058	89
88	1059	90
89	1060	91
90	1061	92
91	1062	93
92	1063	94
93	1064	95
94	1065	96
95	1066	97
96	1067	98
97	1068	99
98	1069	100
99	1070	101
100	1071	102
101	1072	103
102	1073	104
103	1074	105
104	1075	106
105	1076	107

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
106	1077	108
107	1078	109
108	1079	110
109	1080	111
110	1081	112
111	1082	113
112	1083	114
113	1084	115
114	1085	116
115	1086	117
116	1087	118
117	1088	119
118	1089	120
119	1090	121
120	1091	122
121	1092	123
122	1093	124
123	1094	125
124	1095	126
125	1096	127
126	1097	128
127	1098	129
128	1099	130
129	1100	131
130	1101	132
131	1102	133
132	1103	134
133	1104	135
134	1105	136
135	1106	137
136	1107	138
137	1108	139
138	1109	140
139	1110	141
140	1111	142
141	1112	143
142	1113	144
143	1114	145
144	1115	146
145	1116	147
146	1117	148
147	1118	149
148	1119	150
149	1120	151
150	1121	152
151	1122	153
152	1123	154
153	1124	155
154	1125	156
155	1126	157
156	1127	158
157	1128	159
158	1129	160

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
159	1130	161
160	1131	162
161	1132	163
162	1133	164
163	1134	165
164	1135	166
165	1136	167
166	1137	168
167	1138	169
168	1139	170
169	1140	171
170	1141	172
171	1142	173
172	1143	174
173	1144	175
174	1145	176
175	1146	177
176	1147	178
177	1148	179
178	1149	180
179	1150	181
180	1151	182
181	1152	183
182	1153	184
183	1154	185
184	1155	186
185	1156	187
186	1157	188
187	1158	189
188	1159	190
189	1160	191
190	1161	192
191	1162	193
192	1163	194
193	1164	195
194	1165	196
195	1166	197
196	1167	198
197	1168	199
198	1169	200
199	1170	201
200	1171	202
201	1172	203
202	1173	204
203	1174	205
204	1175	206
205	1176	207
206	1177	208
207	1178	209
208	1179	210
209	1180	211
210	1181	212
211	1182	213

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
212	1183	214
213	1184	215
214	1185	216
215	1186	217
216	1187	218
217	1188	219
218	1189	220
219	1190	221
220	1191	222
221	1192	223
222	1193	224
223	1194	225
224	1195	226
225	1196	227
226	1197	228
227	1198	229
228	1199	230
229	1200	231
230	1201	232
231	1202	233
232	1203	234
233	1204	235
234	1205	236
235	1206	237
236	1207	238
237	1208	239
238	1209	240
239	1210	241
240	1211	242
241	1212	243
242	1213	244
243	1214	245
244	1215	246
245	1216	247
246	1217	248
247	1218	249
248	1219	250
249	1220	251
250	1221	252
251	1222	253
252	1223	254
253	1224	255
254	1225	256
255	1226	257
256	1227	258
257	1228	259
258	1229	260
259	1230	261
260	1231	262
261	1232	263
262	1233	264
263	1234	265
264	1235	266

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
265	1236	267
266	1237	268
267	1238	269
268	1239	270
269	1240	271
270	1241	272
271	1242	273
272	1243	274
273	1244	275
274	1245	276
275	1246	277
276	1247	278
277	1248	279
278	1249	280
279	1250	281
280	1251	282
281	1252	283
282	1253	284
283	1254	285
284	1255	286
285	1256	287
286	1257	288
287	1258	289
288	1259	290
289	1260	291
290	1261	292
291	1262	293
292	1263	294
293	1264	295
294	1265	296
295	1266	297
296	1267	298
297	1268	299
298	1269	300
299	1270	301
300	1271	302
301	1272	303
302	1273	304
303	1274	305
304	1275	306
305	1276	307
306	1277	308
307	1278	309
308	1279	310
309	1280	311
310	1281	312
311	1282	313
312	1283	314
313	1284	315
314	1285	316
315	1286	317
316	1287	318
317	1288	319

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
318	1289	320
319	1290	321
320	1291	322
321	1292	323
322	1293	324
323	1294	325
324	1295	326
325	1296	327
326	1297	328
327	1298	329
328	1299	330
329	1300	331
330	1301	332
331	1302	333
332	1303	334
333	1304	335
334	1305	336
335	1306	337
336	1307	338
337	1308	339
338	1309	340
339	1310	341
340	1311	342
341	1312	343
342	1313	344
343	1314	345
344	1315	346
345	1316	347
346	1317	348
347	1318	349
348	1319	350
349	1320	351
350	1321	352
351	1322	353
352	1323	354
353	1324	355
354	1325	356
355	1326	357
356	1327	358
357	1328	359
358	1329	360
359	1330	361
360	1331	362
361	1332	363
362	1333	364
363	1334	365
364	1335	366
365	1336	367
366	1337	368
367	1338	369
368	1339	370
369	1340	371
370	1341	372

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
371	1342	373
372	1343	374
373	1344	375
374	1345	376
375	1346	377
376	1347	378
377	1348	379
378	1349	380
379	1350	381
380	1351	382
381	1352	383
382	1353	384
383	1354	385
384	1355	386
385	1356	387
386	1357	388
387	1358	389
388	1359	390
389	1360	391
390	1361	392
391	1362	393
392	1363	394
393	1364	395
394	1365	396
395	1366	397
396	1367	398
397	1368	399
398	1369	400
399	1370	401
400	1371	402
401	1372	403
402	1373	404
403	1374	405
404	1375	406
405	1376	407
406	1377	408
407	1378	409
408	1379	410
409	1380	411
410	1381	412
411	1382	413
412	1383	414
413	1384	415
414	1385	416
415	1386	417
416	1387	418
417	1388	419
418	1389	420
419	1390	421
420	1391	422
421	1392	423
422	1393	424
423	1394	425

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
424	1395	426
425	1396	427
426	1397	428
427	1398	429
428	1399	430
429	1400	431
430	1401	432
431	1402	433
432	1403	434
433	1404	435
434	1405	436
435	1406	437
436	1407	438
437	1408	439
438	1409	440
439	1410	441
440	1411	442
441	1412	443
442	1413	444
443	1414	445
444	1415	446
445	1416	447
446	1417	448
447	1418	449
448	1419	450
449	1420	451
450	1421	452
451	1422	453
452	1423	454
453	1424	455
454	1425	456
455	1426	457
456	1427	458
457	1428	459
458	1429	460
459	1430	461
460	1431	462
461	1432	463
462	1433	464
463	1434	465
464	1435	466
465	1436	467
466	1437	468
467	1438	469
468	1439	470
469	1440	471
470	1441	472
471	1442	473
472	1443	474
473	1444	475
474	1445	476
475	1446	477
476	1447	478

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
477	1448	479
478	1449	480
479	1450	481
480	1451	482
481	1452	483
482	1453	484
483	1454	485
484	1455	486
485	1456	487
486	1457	488
487	1458	489
488	1459	490
489	1460	491
490	1461	492
491	1462	493
492	1463	494
493	1464	495
494	1465	496
495	1466	497
496	1467	498
497	1468	499
498	1469	500
499	1470	501
500	1471	502
501	1472	503
502	1473	504
503	1474	505
504	1475	506
505	1476	507
506	1477	508
507	1478	509
508	1479	510
509	1480	511
510	1481	512
511	1482	513
512	1483	514
513	1484	515
514	1485	516
515	1486	517
516	1487	518
517	1488	519
518	1489	520
519	1490	521
520	1491	522
521	1492	523
522	1493	524
523	1494	525
524	1495	526
525	1496	527
526	1497	528
527	1498	529
528	1499	530
529	1500	531

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
530	1501	532
531	1502	533
532	1503	534
533	1504	535
534	1505	536
535	1506	537
536	1507	538
537	1508	539
538	1509	540
539	1510	541
540	1511	542
541	1512	543
542	1513	544
543	1514	545
544	1515	546
545	1516	547
546	1517	548
547	1518	549
548	1519	550
549	1520	551
550	1521	552
551	1522	553
552	1523	554
553	1524	555
554	1525	556
555	1526	557
556	1527	558
557	1528	559
558	1529	560
559	1530	561
560	1531	562
561	1532	563
562	1533	564
563	1534	565
564	1535	566
565	1536	567
566	1537	568
567	1538	569
568	1539	570
569	1540	571
570	1541	572
571	1542	573
572	1543	574
573	1544	575
574	1545	576
575	1546	577
576	1547	578
577	1548	579
578	1549	580
579	1550	581
580	1551	582
581	1552	583
582	1553	584

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
583	1554	585
584	1555	586
585	1556	587
586	1557	588
587	1558	589
588	1559	590
589	1560	591
590	1561	592
591	1562	593
592	1563	594
593	1564	595
594	1565	596
595	1566	597
596	1567	598
597	1568	599
598	1569	600
599	1570	601
600	1571	602
601	1572	603
602	1573	604
603	1574	605
604	1575	606
605	1576	607
606	1577	608
607	1578	609
608	1579	610
609	1580	611
610	1581	612
611	1582	613
612	1583	614
613	1584	615
614	1585	616
615	1586	617
616	1587	618
617	1588	619
618	1589	620
619	1590	621
620	1591	622
621	1592	623
622	1593	624
623	1594	625
624	1595	626
625	1596	627
626	1597	628
627	1598	629
628	1599	630
629	1600	631
630	1601	632
631	1602	633
632	1603	634
633	1604	635
634	1605	636
635	1606	637

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
636	1607	638
637	1608	639
638	1609	640
639	1610	641
640	1611	642
641	1612	643
642	1613	644
643	1614	645
644	1615	646
645	1616	647
646	1617	648
647	1618	649
648	1619	650
649	1620	651
650	1621	652
651	1622	653
652	1623	654
653	1624	655
654	1625	656
655	1626	657
656	1627	658
657	1628	659
658	1629	660
659	1630	661
660	1631	662
661	1632	663
662	1633	664
663	1634	665
664	1635	666
665	1636	667
666	1637	668
667	1638	669
668	1639	670
669	1640	671
670	1641	672
671	1642	673
672	1643	674
673	1644	675
674	1645	676
675	1646	677
676	1647	678
677	1648	679
678	1649	680
679	1650	681
680	1651	682
681	1652	683
682	1653	684
683	1654	685
684	1655	686
685	1656	687
686	1657	688
687	1658	689
688	1659	690

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
689	1660	691
690	1661	692
691	1662	693
692	1663	694
693	1664	695
694	1665	696
695	1666	697
696	1667	698
697	1668	699
698	1669	700
699	1670	701
700	1671	702
701	1672	703
702	1673	704
703	1674	705
704	1675	706
705	1676	707
706	1677	708
707	1678	709
708	1679	710
709	1680	711
710	1681	712
711	1682	713
712	1683	714
713	1684	715
714	1685	716
715	1686	717
716	1687	718
717	1688	719
718	1689	720
719	1690	721
720	1691	722
721	1692	723
722	1693	724
723	1694	725
724	1695	726
725	1696	727
726	1697	728
727	1698	729
728	1699	730
729	1700	731
730	1701	732
731	1702	733
732	1703	734
733	1704	735
734	1705	736
735	1706	737
736	1707	738
737	1708	739
738	1709	740
739	1710	741
740	1711	742
741	1712	743

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
742	1713	744
743	1714	745
744	1715	746
745	1716	747
746	1717	748
747	1718	749
748	1719	750
749	1720	751
750	1721	752
751	1722	753
752	1723	754
753	1724	755
754	1725	756
755	1726	757
756	1727	758
757	1728	759
758	1729	760
759	1730	761
760	1731	762
761	1732	763
762	1733	764
763	1734	765
764	1735	766
765	1736	767
766	1737	768
767	1738	769
768	1739	770
769	1740	771
770	1741	772
771	1742	773
772	1743	774
773	1744	775
774	1745	776
775	1746	777
776	1747	778
777	1748	779
778	1749	780
779	1750	781
780	1751	782
781	1752	783
782	1753	784
783	1754	785
784	1755	786
785	1756	787
786	1757	788
787	1758	789
788	1759	790
789	1760	791
790	1761	792
791	1762	793
792	1763	794
793	1764	795
794	1765	796

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
795	1766	797
796	1767	798
797	1768	799
798	1769	800
799	1770	801
800	1771	802
801	1772	803
802	1773	804
803	1774	805
804	1775	806
805	1776	807
806	1777	808
807	1778	809
808	1779	810
809	1780	811
810	1781	812
811	1782	813
812	1783	814
813	1784	815
814	1785	816
815	1786	817
816	1787	818
817	1788	819
818	1789	820
819	1790	821
820	1791	822
821	1792	823
822	1793	824
823	1794	825
824	1795	826
825	1796	827
826	1797	828
827	1798	829
828	1799	830
829	1800	831
830	1801	832
831	1802	833
832	1803	834
833	1804	835
834	1805	836
835	1806	837
836	1807	838
837	1808	839
838	1809	840
839	1810	841
840	1811	842
841	1812	843
842	1813	844
843	1814	845
844	1815	846
845	1816	847
846	1817	848
847	1818	849

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
848	1819	850
849	1820	851
850	1821	852
851	1822	853
852	1823	854
853	1824	855
854	1825	856
855	1826	857
856	1827	858
857	1828	859
858	1829	860
859	1830	861
860	1831	862
861	1832	863
862	1833	864
863	1834	865
864	1835	866
865	1836	867
866	1837	868
867	1838	869
868	1839	870
869	1840	871
870	1841	872
871	1842	873
872	1843	874
873	1844	875
874	1845	876
875	1846	877
876	1847	878
877	1848	879
878	1849	880
879	1850	881
880	1851	882
881	1852	883
882	1853	884
883	1854	885
884	1855	886
885	1856	887
886	1857	888
887	1858	890
888	1859	891
889	1860	892
890	1861	893
891	1862	894
892	1863	895
893	1864	896
894	1865	897
895	1866	898
896	1867	899
897	1868	900
898	1869	901
899	1870	902
900	1871	903

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
901	1872	904
902	1873	905
903	1874	906
904	1875	907
905	1876	908
906	1877	909
907	1878	910
908	1879	911
909	1880	912
910	1881	913
911	1882	914
912	1883	915
913	1884	916
914	1885	917
915	1886	918
916	1887	919
917	1888	920
918	1889	921
919	1890	922
920	1891	923
921	1892	924
922	1893	925
923	1894	926
924	1895	927
925	1896	928
926	1897	929
927	1898	930
928	1899	931
929	1900	932
930	1901	933
931	1902	934
932	1903	935
933	1904	936
934	1905	937
935	1906	938
936	1907	939
937	1908	940
938	1909	941
939	1910	942
940	1911	943
941	1912	944
942	1913	945
943	1914	946
944	1915	947
945	1916	948
946	1917	949
947	1918	950
948	1919	951
949	1920	952
950	1921	953
951	1922	954
952	1923	955
953	1924	956

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Table 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/324,631
954	1925	957
955	1926	958
956	1927	959
957	1928	960
958	1929	961
959	1930	962
960	1931	963
961	1932	964
962	1933	965
963	1934	966
964	1935	967
965	1936	968
966	1937	969
967	1938	970
968	1939	971
969	1940	972
970	1941	973
971	1942	974

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-971.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 99% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-971.

11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of any of the polynucleotides from SEQ ID NO: 1-971, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 972-1942.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising of at least one of SEQ ID NO: 1-971.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.